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UTILITY PATENT APPLICATION TRANSMITTAL AND FEE SHEET

Transmitted herewith for filing under 37 CFR §1.53(b)(1) is a **divisional** of prior Application No. 09/001,982, filed December 31, 1997.

Applicant (or identifier): BOSCH ET AL.

Title: GENES ENCODING HYBRID *BACILLUS THURINGIENSIS* TOXINS

Enclosed are:

1. ☒ Specification (Including Claims and Abstract) - 92 pages
2. ☒ Drawings - 7 sheets (formal)
3. Declaration and Power of Attorney
   a. ☐ Newly executed (original or copy)
   b. ☒ Copy from a prior application (signed or with indication that original was signed)
      i. ☐ Deletion of Inventors
      Signed statement attached deleting inventor(s) named in the prior application
4. ☒ Incorporation By Reference
   The entire disclosure of the prior application, from which a copy of the Declaration and Power of Attorney is supplied under Box 3b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
5. ☐ Microfiche Computer Program (appendix)
6. Nucleotide and/or Amino Acid Sequence Submission
   ☒ Computer Readable Copy
   ☒ Paper Copy
   ☒ Statement Verifying Identity of Above Copies
7. ☒ Preliminary Amendment
8. ☐ Assignment Papers (Cover Sheet & Document(s))
9. ☐ English Translation of
10. ☒ Information Disclosure Statement
11. ☐ Certified Copy of Priority Document(s)
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13. ☒ Other: Bibliographic Data Sheet

☒ The right to elect an invention or species that is different from that elected in parent Application No. 09/001,982 in the event of a restriction or election of species requirement that is identical or substantially similar to that made in said parent application is hereby reserved.

Filing fee calculation:

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Basic Filing Fee								$	690
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Extra Claims	Total Claims	29	-20	9	x	$ 18	=	$	162
	Independent Claims	1	-3	0	x	$ 78	=	$	
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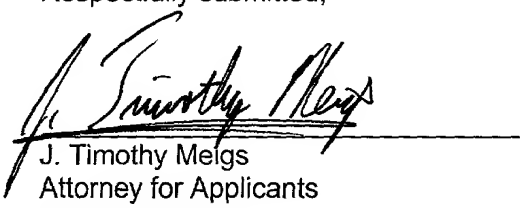
Respectfully submitted,



Date: September 22, 2000

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CORRESPONDENCE INFORMATION

Correspondence Customer Number:: 022847

APPLICATION INFORMATION

Title Line One:: Genes Encoding Hybrid Bacillus thuringie
Title Line Two:: nsis Toxins
Total Drawing Sheets:: 7
Formal Drawings?:: Yes
Application Type:: Utility
Docket Number:: S-130-4080C
Secrecy Order in Parent Appl.?:: No

CONTINUITY INFORMATION

This application is a:: DIVISION OF
> Application One:: 09/001,982
Filing Date:: 12-31-1997

Which is a:: CONTINUATION IN PART OF
>> Application Two:: 08/602,737
Filing Date:: 02-21-1996
Patent Number:: 5736131

Which is a:: 371 OF
>>> Application Three:: EP94/02909
Filing Date:: 09-01-1994

PRIOR FOREIGN APPLICATIONS

Foreign Application One:: 9318207.9
Filing Date:: 09-02-1993
Country:: Great Britain
Priority Claimed:: Yes

Source:: PrintEFS Version 1.0.1

CASE S-130-4080C

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF

BOSCH ET AL.

APPLICATION NO: TBA

FILED: SEPTEMBER 22, 2000

FOR: GENES ENCODING HYBRID *BACILLUS THURINGIENSIS* TOXINS (AS AMENDED)

Assistant Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Sir:

Applicants respectfully request that the above-captioned application be amended as follows in advance of examination:

IN THE SPECIFICATION

Please change the title to -- Genes Encoding Hybrid *Bacillus thuringiensis* Toxins --.

Please replace the continuing data beneath the title with the following: -- This application is a division of application no. 09/001,982, filed December 31, 1997, which is a continuation-in-part of application no. 08/602,737, filed February 21, 1996, now U.S. Patent No. 5,736,131, which is a § 371 of international application no. PCT/EP94/02909, filed September 1, 1994. The aforementioned applications are incorporated herein by reference. --.

IN THE CLAIMS

Please cancel claims 1-16, 18-20, 29-31, 35-40 without prejudice or disclaimer.

Please amend claims 17 and 21 as follows:

17. (Amended) An isolated DNA molecule encoding [a protein that comprises the amino acid sequence of the hybrid toxin fragment of claim 1.] a polypeptide comprising an insecticidal *Bacillus thuringiensis* hybrid toxin fragment, comprising:

a) at a C-terminus of said fragment, domain III of a first Cry protein; and

b) at an N-terminus of said fragment, domains I and II of a second Cry protein different from the first Cry protein.

21. (Amended) An isolated [*Bacillus thuringiensis* hybrid toxin fragment] DNA molecule according to claim [1] 17, wherein said hybrid toxin fragment binds to a binding site in an insect gut that is different than the site bound by said first Cry protein.

Please add new claims 41-57 as follows:

41. An isolated DNA molecule according to claim 17, wherein said first Cry protein is CryIC.

42. An isolated DNA molecule according to claim 17, wherein said second Cry protein is selected from the group consisting of CryIA, CryIE, and CryIG.

43. An isolated DNA molecule according to claim 42, wherein said second Cry protein is CryIA.

44. An isolated DNA molecule according to claim 42, wherein said second Cry protein is CryIE.

45. An isolated DNA molecule according to claim 42, wherein said second Cry protein is CryIG.

46. An isolated DNA molecule according to claim 17, wherein said first Cry protein is CryIC, and wherein said second Cry protein is CryIA, CryIE, or CryIG.

47. An isolated DNA molecule according to claim 17, wherein said C-terminus comprises the sequence from amino acid position 454 to position 602 of SEQ ID NO:2.

48. An isolated DNA molecule according to claim 17, wherein said C-terminus comprises the sequence from amino acid position 478 to position 602 of SEQ ID NO:2.

49. An isolated DNA molecule according to claim 17, wherein said insecticidal *Bacillus thuringiensis* hybrid toxin fragment comprises an amino acid sequence at least 90% similar to amino acids 1-620 of SEQ ID NO:6.

50. An isolated DNA molecule according to claim 17, wherein said insecticidal *Bacillus thuringiensis* hybrid toxin fragment comprises an amino acid sequence at least 90% similar to amino acids 1-627 of SEQ ID NO:8.

51. An isolated DNA molecule according to claim 17, wherein said insecticidal *Bacillus thuringiensis* hybrid toxin fragment comprises an amino acid sequence at least 90% similar to amino acids 1-602 of SEQ ID NO:12.

52. An isolated DNA molecule according to claim 17, comprising a nucleotide sequence that hybridizes to nucleotides 1-1860 of SEQ ID NO:5 under the following set of conditions: hybridization at 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C; wash with 2X SSC, 1% SDS, at 50°C.

53. An isolated DNA molecule according to claim 17, comprising a nucleotide sequence that hybridizes to nucleotides 1-1881 of SEQ ID NO:7 under the following set of conditions: hybridization at 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C; wash with 2X SSC, 1% SDS, at 50°C.

54. An isolated DNA molecule according to claim 17, comprising a nucleotide sequence that hybridizes to nucleotides 1-1806 of SEQ ID NO:11 under the following set of conditions: hybridization at 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C; wash with 2X SSC, 1% SDS, at 50°C.

55. An isolated DNA molecule according to claim 17, comprising a nucleotide sequence that is at least 90% identical to nucleotides 1-1860 of SEQ ID NO:5.

56. An isolated DNA molecule according to claim 17, comprising a nucleotide sequence that is at least 90% identical to nucleotides 1-1881 of SEQ ID NO:7.

57. An isolated DNA molecule according to claim 17, comprising a nucleotide sequence that is at least 90% identical to nucleotides 1-1806 of SEQ ID NO:11.

REMARKS

The title has been changed to more accurately reflect what is being claimed. The continuing data has also been updated. Claims 1-16, 18-20, 29-31, 35-40 have been canceled; claims 17 and 21 have been amended; and new claims 41-57 have been added. Thus, the pending claims are 17, 21-28, 32-34, and 41-57.

Applicants note that claim 17 (now the sole independent claim) has been amended to recite the encoded hybrid *Bt* toxin using language identical to that in allowed claim 1 of parent application no. 09/001,982. Thus, it is believed that claim 17 of the instant application is allowable as amended. The

remaining claims in the instant application all depend either directly or indirectly from amended claim 17. Hence, it is believed that they too are in condition for allowance.

Applicants respectfully request that the instant amendment be entered and receive favorable consideration. The Examiner is invited to telephone the undersigned attorney if any questions or concerns arise during examination of the pending claims.

Respectfully submitted,

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Date: September 22, 2000

HYBRID TOXIN

This application is a continuation-in-part of application serial no. 08/602,737, filed February 21, 1996, which is a 371 of international application no. PCT/EP94/02909, filed September 1, 1994. Both of the aforementioned applications are incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates to hybrid toxin fragments, and toxins comprising them, derived from *Bacillus thuringiensis* insecticidal crystal proteins.

BACKGROUND OF THE INVENTION

Bacillus thuringiensis (hereinafter B.t.) is capable of producing proteins that accumulate intra-cellularly as crystals. These crystal proteins are toxic to a number of insect larvae. Based on sequence homology and insecticidal specificity, crystal proteins have been categorized into different classes. Best studied are the CryI class of proteins, which are produced as 140 kDa protoxins and are active towards lepidopterans.

To some extent, the mode of action of crystal proteins has been elucidated. After oral uptake, the crystals dissolve in the alkaline environment of the larval midgut. The solubilized proteins are subsequently processed by midgut proteinases to a proteinase-resistant toxic fragment of about 65kDa, which binds to receptors on epithelial cells of the insect midgut and penetrates the cell membrane. This eventually leads to bursting of the cells and death of the larvae.

The activity spectrum of a particular crystal protein is to a large extent determined by the occurrence of receptors on the midgut epithelial cells of susceptible insects. The activity spectrum is co-determined by the efficiency of solubilization of the crystal protein and its proteolytic activation *in vivo*.

The importance of the binding of the crystal protein to midgut epithelial receptors is further demonstrated where insects have developed resistance to one of the crystal proteins, such that the binding of crystal proteins to midgut epithelial cells in resistant insects is significantly reduced.

Toxic fragments of crystal proteins are thought to be composed of three distinct structural domains. Domain I, the most N-terminal domain, consists of 7 a-helices. Domain II comprises 3 ß-sheets. Domain III, the most C-terminal domain, folds into a ß-sandwich. If projected on CryI sequences, domain I runs from about amino acid residues 28 to 260, domain II from about 260 to 460, and domain III from about 460 to 600.

DESCRIPTION OF THE INVENTION

The present invention concerns hybrid crystal proteins particularly, though not exclusively, involving CryIC together with CryIE, CryIA, or CryIG. The nucleotide sequence of the CryIC gene from B.t. sub. sp. *entomocidus* 60.5 is given in SEQ ID NO:1, and the corresponding amino acid sequence of the protein encoded by said nucleotide sequence is given in SEQ ID NO:2. The nucleotide sequence of the CryIE gene from B.t. sub. sp. *kenyae* 4FI is given in SEQ ID NO:3, and the corresponding amino acid sequence of the protein encoded by said nucleotide sequence is given in SEQ ID NO:4. The nucleotide sequence of a B.t. CryIG gene is given in SEQ ID NO:9, and the corresponding amino acid sequence of the protein encoded by said nucleotide sequence is given in SEQ ID NO:10. These proteins are toxic to lepidopterans, but within this order of insects, each protein has different specificity. CryIC, for example, is particularly active against *S. exigua* and *M. brassicae*.

According to the present invention, there is provided an isolated B.t. hybrid toxin fragment comprising at its C-terminus domain III of a first Cry protein, or a part of said domain or a protein substantially similar to said domain; and comprising at its N-terminus the N-terminal region of a second Cry protein, or a part of said region or a protein substantially similar to said region. For example, a preferred B.t. hybrid toxin fragment according to the present invention comprises at its C-terminus domain III of a first Cry protein and comprises at its N-terminus domains I and II of a second Cry protein. A preferred fragment is one that does not bind to the CryIC binding site in an insect gut when it comprises at its C-terminus domain III of CryIC, or a part of said domain or a protein substantially similar to said domain; or one that does not bind to a CryIA binding site when it comprises at its C-terminus domain III of CryIA, or a part of said domain or a protein substantially similar to said domain.

In the context of the present invention, "substantially similar" means a pure protein having an amino acid sequence that is at least 75% similar to the sequence of a protein according to the invention. It is preferred that the degree of similarity is at least 85%, more preferred that the degree of similarity is at least 90%, and still more preferred that the degree of similarity is at least 95%. In the context of the present invention, two amino acid sequences with at least 75%, 85%, 90%, or 95% similarity to each other have at least 75%, 85%, 90%, or 95% identical or conservatively replaced amino acid residues in a like position when aligned optimally allowing for up to 6 gaps, with the proviso that, with respect to the gaps, a total not more than 15 amino acid residues are affected. For the purpose of the present invention, conservative replacements may be made between amino acids within the following groups:

(i) Serine and Threonine;

(ii) Glutamic acid and Aspartic acid;

(iii) Arginine and Lysine;

(iv) Asparagine and Glutamine;

(v) Isoleucine, Leucine, Valine, and Methionine;

(vi) Phenylalanine, Tyrosine, and Tryptophan; and

(vii) Alanine and Glycine,

with the proviso that in SEQ ID NO:6, Ser and Tyr are conservative replacements at position 620, and Ala and Glu are conservative replacements at position 618; and that in SEQ ID NO:8, Ser and Tyr are conservative replacements at position 627, and Ala and Glu are conservative replacements at position 625.

In the context of the present invention, "part" of a protein means a peptide comprised by said protein and having at least 80% of the consecutive sequence thereof.

In the context of the present invention, "binding site" means a site on a molecule wherein the binding between site and toxin is reversible such that the *Ka* between site and toxin is in the order of at least $10^4 dm^3 mole^{-1}$.

The toxin fragment may comprise at its N-terminus the N-terminal region of any insecticidal protein from B.t. being commonly known as "Cry" or "Cyt", including: CryIA(a),

CryIA(b) CryIA(c), CryIB, CryIC, CryID, CryIE, CryIF, CryIG, CryIH, CryIIA, CryIIB, CryIIC, CryIIIA, CryIIIB, CryIIIB(b), CryIVA, CryIVB, CryIVC, CryIVD, CYTA, CryX1(IIIC), CryX2(IIID), CryX3, CryV, and CryX4, or a part of said region or a protein substantially similar to said region. The toxin fragment may comprise at its C-terminus domain III of CryIC, or a part of said domain or a protein substantially similar to said domain.

Thus, the fragment may comprise domain II of CryIE, CryIB, CryID, CryIA, or CryIG, or a part of said domain II or a protein substantially similar to said domain II, and domain III of CryIC or a part of said domain III or a protein substantially similar to said domain III. It is particularly preferred that the fragment comprises domains I and II of CryIE, CryIB, CryID, CryIA, or CryIG, or a part thereof or a protein substantially similar to said domains I and II, and domain III of CryIC or a part thereof or a protein substantially similar to said domain III.

It is most preferred that the toxin fragment comprises a region at its C-terminus comprising the sequence from amino acid position 454 to position 602 of CryIC, or a sequence substantially similar to said sequence. The fragment may comprise a region at its C-terminus comprising the sequence from amino acid position 478 to 602 of Cry IC, or a sequence substantially similar to said sequence, with the proviso that if the sequence comprising amino acids 478 to 602 of CryIC is fused directly to the C-terminus of domain II of CryIA, CryIB, CryID, CryIE, or CryIG, then the folding of the fusion product is satisfactory to yield an insecticidal component of the fragment. The routineer in the art will recognize that it may be necessary to add a peptide region to the C-terminus of domain II that spaces the C-terminal region of CryIC apart, thus enabling it to fold in such a way as to exhibit insecticidal activity.

It is most particularly preferred that the toxin fragment according to the invention comprises one of the following:

i) an amino acid sequence from about amino acid 1 to about amino acid 620 in SEQ ID NO:6, or an amino acid sequence from about amino acid 1 to about amino acid 620 in SEQ ID NO:6, wherein with respect to said sequence, at least one of the following alterations is present:

Ile at position 609 is replaced with Leu,

Ala at position 618 is replaced with Glu,

Ser at position 620 is replaced with Tyr;

ii) an amino acid sequence from about amino acid 1 to about amino acid 627 in SEQ ID NO:8, or an amino acid sequence from about amino acid 1 to about amino acid 627 in SEQ ID NO:8, wherein with respect to said sequence, at least one of the following alterations is present:

Ile at position 616 is replaced with Leu,

Ala at position 625 is replaced with Glu,

Ser at position 627 is replaced with Tyr; and

iii) an amino acid sequence from about amino acid 1 to about amino acid 602 in SEQ ID NO:12.

Whatever amino acid alterations are permitted, however, one or more of the following residues indicated sequence-wise with respect to the CryIC sequence is invariable: Phe (501), Val (478), Trp (479), and Thr (486).

The invention also includes a hybrid toxin comprising the above disclosed fragment or a toxin at least 85% similar to such a hybrid toxin, which has substantially similar insecticidal activity or receptor binding properties.

The invention still further includes pure proteins that are at least 90% similar to the toxin fragments or hybrid toxins according to the invention.

The invention still further includes recombinant DNA comprising a sequence encoding a protein comprising an amino acid sequence of one of the above-disclosed toxins or fragments thereof. The invention still further includes recombinant DNA comprising the sequence from about nucleotide 1 to about nucleotide 1860 given in SEQ ID NO:5, or DNA similar thereto encoding a substantially similar protein; or recombinant DNA comprising the sequence from about nucleotide 1 to about nucleotide 1881 in SEQ ID NO:7, or DNA similar thereto encoding a substantially similar protein; or recombinant DNA comprising the sequence from about nucleotide 1 to about nucleotide 1806 in SEQ ID NO:11, or DNA similar thereto encoding a substantially similar protein.

In the context of the present invention, "similar DNA" means a test sequence that is capable of hybridizing to the inventive recombinant sequence. When the test and inventive sequences are

double stranded, the nucleic acid constituting the test sequence preferably has a TM within 20°C of that of the inventive sequence. In the case that the test and inventive sequences are mixed together and denatured simultaneously, the TM values of the sequences are preferably within 10°C of each other. More preferably, the hybridization is performed under stringent conditions, with either the test or inventive DNA preferably being supported. Thus, either a denatured test or inventive sequence is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of between 50 and 70°C in double strength citrate buffered saline containing 0.1% SDS, followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required, and thus the degree of similarity of the sequences, such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one tenth strength SC containing 0.1% SDS. Sequences having the greatest degree of similarity are those the hybridization of which is least affected by washing in buffers of reduced concentration. It is most preferred that the test and inventive sequences are so similar that the hybridization between them is substantially unaffected by washing or incubation in one tenth strength sodium citrate buffer containing 0.1% SDS. Typical stringent conditions are as follows: hybridization at 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C; wash with 2X SSC, 1% SDS, at 50°C.

The recombinant DNA may further encode a protein having herbicide resistance, plant growth-promoting, anti-fungal, anti bacterial, anti-viral, and/or anti-nematode properties. In the case that the DNA is to be introduced into a heterologous organism, it may be modified to remove known mRNA instability motifs (such as AT rich regions) and polyadenylation signals, and/or codons that are preferred by the organism into which the recombinant DNA is to be inserted may be used so that expression of the thus modified DNA in the organism yields substantially similar protein to that obtained by expression of the unmodified recombinant DNA in the organism in which the protein components of the hybrid toxin or toxin fragments are endogenous.

The invention still further includes a DNA sequence complementary to one that hybridizes under stringent conditions with the recombinant DNA according to the invention.

Also included in the present invention are the following: a vector containing such a recombinant (or complementary thereto) DNA sequence; a plant or microorganism that includes and enables expression of such DNA; plants transformed with such DNA; the progeny of such plants that contain the DNA stably incorporated and hereditable in a Mendelian manner; and/or the seeds of such plants and such progeny.

The invention still further includes protein derived from expression of the recombinant DNA of the invention, and insecticidal protein produced by expression of the recombinant DNA within plants transformed therewith.

The invention still further includes the following: an insecticidal composition containing one or more of the toxin fragments or toxins comprising them according to the invention; a process for combating insects that comprises exposing them to such fragments or toxins or compositions; and an extraction process for obtaining insecticidal proteins from organic material containing them, comprising submitting the material to maceration and solvent extraction.

DESCRIPTION OF THE FIGURES

Figure 1 shows the generation of hybrid crystal protein genes via *in vivo* recombination. Tandem plasmids (pBD560 and pBD 650) carrying two truncated crystal protein genes in direct repeat orientation are constructed. The 5' located gene (open bar) lacks the protoxin encoding region (solid bar) and of the 3' located gene (dashed bar) part of the domain I encoding region is deleted. *In vivo* recombination between homologous regions (domain II and III) occurs in *rec*A + strain JM101. Selection against non-recombinants by digestion with *Not*I and *Bam*HI and subsequent transformation results in sets of plasmids encoding hybrid crystal proteins.

Figure 2 shows the alignment of amino acid residues 420 to 630 of CryIE and CryIC. The border between domain II and III is indicated. Only amino acid residues of CryIC that differ from CryIE are depicted; identical residues are indicated by dots. The crossover positions (G27, H13, H7, H8, H17, and H21) in the CryIE/CryIC hybrid toxin fragments according to the invention are indicated on the Figure.

Figure 3 shows the alignment of amino acid residues 420 to 630 of CryIE and CryIC. The border between domain II and III is indicated. Only amino acid residues of CryIC that differ from CryIE are depicted; identical residues are indicated by dots. The crossover positions (F59, F71, F26, and E7) in the CryIC/CryIE hybrid toxin fragments are indicated on the Figure.

Figure 4 shows the results of heterologous competition experiments. Biotinylated CryIC (panel A) and G27 (panel B) are incubated with *S. exigua* BBMV vesicles in the absence (lanes a) or presence of an excess of unlabelled protein as indicated. After the incubation, the vesicles are washed, loaded on a SDS-polyacrylamide gel and blotted to a nitrocellulose membrane. Biotinylated crystal proteins, re-isolated with the vesicles, are visualized using streptavidin-peroxidase conjugate and are indicated on the Figure with an arrow head.

Figure 5 shows the plasmid map of pSB456, which encodes the G27 hybrid toxin fragment and is used to transform the crystal toxin minus strain B.t. 51.

Figure 6A shows the alignment of the *cry1G* and *cry1C* genes with the crossover points of the *cry1G/cry1C* hybrids. The position relative to the first nucleotide of the start codon of *cry1G* is shown.

Figure 6B shows the alignment of the encoded Cry1G and Cry1C proteins with the crossover points of the Cry1G/Cry1C hybrids. The approximate position of the domain II-III border is indicated by #. The position relative to the initiation codon of Cry1G is also indicated.

Figure 7 shows the results of assays measuring the toxicity of Cry1G/Cry1C hybrid toxins towards *Spodoptera exigua*.

DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

SEQ ID NO:1 shows the nucleotide sequence of the CryIC gene from B.t. sub. sp. *entomocidus* 60.5.

SEQ ID NO:2 shows the amino acid sequence of the protein encoded by the CryIC gene shown in SEQ ID NO:1.

SEQ ID NO:3 shows the nucleotide sequence of the CryIE gene from B.t. sub. sp. *kenyae* 4FI.

SEQ ID NO:4 shows the amino acid sequence of the protein encoded by the CryIE gene shown in SEQ ID NO:3.

SEQ ID NO:5 shows the nucleotide sequence encoding a preferred CryIE/CryIC B.t. hybrid toxin fragment according to the invention.

SEQ ID NO:6 shows the amino acid sequence of the protein encoded by the nucleotide sequence shown in SEQ ID NO:5.

SEQ ID NO:7 shows the nucleotide sequence of a CryIA/CryIC hybrid toxin fragment according to the invention.

SEQ ID NO:8 shows the amino acid sequence of the protein encoded by the nucleotide sequence depicted in SEQ ID NO:7.

SEQ ID NO:9 shows the nucleotide sequence of a B.t. CryIG gene.

SEQ ID NO:10 shows the amino acid sequence of the protein encoded by the CryIG gene shown in SEQ ID NO:9.

SEQ ID NO:11 shows the nucleotide sequence encoding a preferred CryIG/CryIC B.t. hybrid toxin fragment (hybrid HK28-24) according to the invention.

SEQ ID NO:12 shows the amino acid sequence of the protein encoded by the nucleotide sequence shown in SEQ ID NO:12.

SEQ ID NOs:13-15 are oligonucleotides.

The invention will be further apparent from the following non-limiting Examples, which describe the production of B.t. hybrid toxin fragments according to the invention, taken in conjunction with the associated Figures and Sequence Listing.

EXAMPLES

Production Of Plasmids Encoding Hybrid Toxin Fragments

In the production of plasmids carrying the CryIC or CryIE genes, *Escherichia coli* XLI-blue (Stratagene Inc.) is used as plasmid host except in cases were JM101 is used as *rec*A+ background. A vector for the expression of crystal proteins in *E. coli* is derived from pKK233-2 (Pharmacia LKB Biotechnology). The size of pKK233-2 is reduced by deleting an *Eco*RI-*Pvu*II fragment carrying the gene encoding tetracycline resistance. Subsequently a 6 bp *Xho*I linker is ligated into the *Hind*III site resulting in pBD10. Plasmid BK+ is created by insertion of a *Bgl*II linker in the *Sac*I site of Bluescript SK+ (Stratagene Inc.). The polylinker of BK+ from *Bgl*II to *Xho*I is introduced between the *Nco*I-*Xho*I site in pBD10. The resulting expression vector pBD11 contains the highly expressed *trc* promoter, the *lacZ* ribosome binding site and ATG initiation codon. The initiation codon overlaps with a *Nco*I site and is followed by the polylinker to facilitate insertions into the vector. Transcription is terminated by the *rrn*B transcription terminator.

The cloning of the *cryIC* and *cryIE* genes from B.t. sub. sp. *entomocidus* 60.5 and *kenya* 4F1 respectively is as described previously (Honée *et al.*, 1990 (Appl. Environ. Microbiol. 56, pp. 823-825); Visser *et al.*, 1990 (J. Bacteriol. 172, pp. 6783-6788)). For cloning purposes, an *Nco*I site overlapping with the start codon of *cryIC* is created by *in vitro* mutagenesis. A *Bgl*II site is created directly downstream of the translation termination codon of cryIC by site directed mutagenesis, resulting in the sequence ATAAGATCTGTT (SEQ ID NO:13 - stop-codon underlined). The *Nco*I-*Bgl*II fragment containing the *cryIC* coding region is ligated into pBD11, resulting in CryIC expression plasmid pBD150. pBD155 is a derivative of pBD150, in which the polylinker sequences 3' of *cryIC* are deleted.

A *Dra*I fragment from pEM14 (Visser *et al.*, 1990) containing the complete *cry*IE gene is cloned in the *Eco*RV site of SK+, resulting in plasmid pEM15. Subsequently, an *Nco*I site is introduced by site directed mutagenesis at the start codon of the gene, and *cryIE* is transferred as an *Nco*I-*Xho*I fragment to pBD11, resulting in CryIE expression plasmid pBD160.

Plasmids carrying only toxic fragment-encoding regions of the *cryI* genes are constructed. *Bgl*II linkers are ligated to *Xmn*I sites present at bp position 1835 of *cryIC*, and to the *Hgi*AI site at position 1839 of *cryIE*. Subsequently, *Nco*I-*Bgl*II fragments containing the *cryIC* (1835 bp) and *cryIE* (1839 bp) toxic fragment-encoding regions are ligated into pBD11, resulting in pBD151 and pBD161 respectively as described below.

Tandem plasmids used for the generation of *cryIC-cryIE* hybrid genes are constructed as follows: *BamH*I linkers are ligated to pBD160 digested with *Hpa*I. This DNA is incubated with *BamH*I and *Xho*I and the truncated *cryIE* gene running from bp 704 is ligated into pBD151 resulting in pBD560. To construct a tandem plasmid for the generation of *cryIE-cryIC* hybrids, pBD155 is digested with *Nsi*I and *Xho*I. The fragment carrying the truncated *cryIC* gene, running from bp 266, is ligated into *Pst*I/*Xho*I digested pBD161, resulting in plasmid pBD650. Due to polylinker sequences, unique *Not*I and *Bam*H1 restriction sites are present between the truncated *cryI* genes present in the tandem plasmids pBD560 and pBD650.

DNA Manipulations And Construction Of Hybrid Toxins

All recombinant DNA techniques are as described by Sambrook *et al.* 1989 (in "Molecular Cloning, A Laboratory Manual: Cold Spring Harbour Press, Cold Spring Harbour). DNA sequencing is performed by the dideoxytriphosphate method with fluorescent dyes attached to the dideoxynucleotides. Analysis is automated by using an Applied Biosystems 370A nucleotide sequence analyzer.

The homology present between *cryI* genes permits intramolecular recombination *in vivo*. Two tandem plasmids are created, each carrying two truncated crystal protein genes overlapping only in domains II and III. Therefore, recombination occurs only in regions encoding domains II and III. In-frame recombinations, which can be selected for by restriction enzyme digestion, generate plasmids that express full size 140 kDa hybrid protoxins. To generate *in vivo* recombinants, a tandem plasmid (either pBD560 or pBD650; Figure 2) is transferred to JM101. 5 mg of DNA is isolated from independently generated recombinants and is digested with *Not*I and *Bam*HI cutting between the two truncated *cryI* genes to select against non-recombinants, and the

DNA is transformed to *E. coli* XL1-blue. 5 single colonies are grown and protein patterns and plasmid content are analyzed.

CryIC/CryIE and CryIE/CryIC hybrid toxins are generated using the tandem plasmids pBD560 and pBD650 respectively, which are allowed to recombine in a *recA*+ background. DNA is isolated, digested, and transferred to *recA*- strain as described above.

100 colonies of 20 independent experiments are analyzed on SDS-PAGE. 85% of these clones produce a 140 kDa protein indicating in frame recombinations between *cryIC* and *cryIE*, and *cryIE* and *cryIC*, respectively. In *E. coli*, CryI proteins are produced as crystals that can be solubilized *in vitro* at high pH. Approximately 15% of hybrid toxins produced as above are solubilized at high pH. The recombinants producing soluble hybrid toxins are first classified using restriction enzymes. Subsequently, for each class, the crossover point of selected hybrids is determined by DNA sequence analysis. All crossovers resulting in soluble hybrid toxins occur in or very close to domain III.

Protein Purification And Analysis

Crystal proteins are isolated essentially as described by Convents *et al.* (J. Biol. Chem. 265, pp. 1369-1375; Eur. J. Biochem., 195, pp. 631-635). Briefly, recombinant *E. coli* are grown at 30°C in 250 ml TB medium to an OD_{660} of 10-15. Crystals isolated from the *E.coli* lysate are solubilized during incubation for 2 hours in 20mM Na_2CO_3, 10 mM dithiothreitol, 100 mM NaCl, pH10, at 37°C. The pH of the solution is lowered to 8 with Tris-HCl and incubated with trypsin. The toxin solution is dialysed against 20 mM Tris-HCl, 100 mM, NaCl pH9. Subsequently, the toxic fragment is purified on a Mono Q 5/5 column connected to a fast-protein liquid chromatography (FPLC) system (Pharmacia LKB Biotechnology). Proteins are separated by 7.5% sodium dodecyl sulfate-polyacrylamide gel electrophoreses.

Biochemical Analysis And Isolation Of 65 kDa Toxic Fragments

Isolated crystals of purified CryIC, CryIE, and the hybrid proteins are solubilized at high pH and incubated with trypsin. Like CryIC and CryIE, all soluble hybrid toxins with crossovers in domain III are converted to stable 65 kDa fragments. The 65 kDa fragments can be purified using

anion exchange chromatography under similar conditions as the parental proteins. Hybrids F59 and F71, which have crossovers in domain II, are completely degraded by trypsin. Apparently, although these hybrids do not precipitate as insoluble aggregates, trypsin cleavage sites buried in the parental proteins may become exposed to trypsin. Because of this phenomenon, no 65 kDa fragments are isolated from F59 and F71.

Table 1 shows the constitution of 5 CryIE/CryIC hybrid toxins: (G27, H8, H17, H13, H7, and H21) and 4 CryIC/CryIE hybrid toxins (F59, F71, F26, and E7) with reference to the CryIC and CryIE proteins from which they are derived. The amino acid sequences of the CryIE/CryIC toxins comprising the toxic fragments of the present invention run to amino acid 1189 of the CryIC parent protein. The amino acid sequences of the CryIC/CryIE hybrid toxins run to amino acid 1171 of the CryIE parent protein. Table 1 also shows the relative insecticidal effectiveness of these various hybrid toxins with respect to the CryIC and CryIE proteins.

TABLE 1

Toxin	aa IE	aa IC	*M. sexta*	*S. exigua*	*M. brassicae*
IC	0	28-627	++	++	++
IE	29-612	0	++	-	-
G27	1-474	478-627	++	++(+)	+(+)
H8	1-497	501-627	++	-	-
H17	1-529	533-627	++	-	-
H7	1-577	588-627	-	-	-
H21	1-605	621-627			
F59	421-612	1-423	-	-	-
F71	428-612	1-430	-	-	-
F26	455-612 (1171)	1-458	++	-	-
E7	588-612 (1171)	1-602	++	++	++

Table 1. Constitution and toxicity of hybrid toxins with respect to the parent proteins. Most bioassays were performed with purified toxin fragments. In case of CryIC these run from about aa 28 to about aa 627, and in case of CryIE till 612. The length of complete protoxins is indicated between brackets.

Insect Toxicity Assays And Insecticidal Activity of *cryIC/cryIE* Hybrid Gene Products

Bacterial cultures are concentrated to OD_{660} 6.0, and 100 ml are spotted on 2 cm^2 of artificial diet in a 24-well tissue culture plate. Alternatively, diluted samples of purified toxins are applied to the diet. Second instar larvae of either *S. exigua*, *M. brassicae,* or *M. sexta* are fed on this diet (16 per sample dilution) for 5 days, after which the larval weight is scored. The relative growth (EC50, the concentration giving 50% growth reduction) is determined by calculating the ratio between the mean weight of larvae grown on diet supplemented with toxin and the mean weight of control larvae grown on a diet without toxin. *M. sexta* egg layers are supplied by Carolina Biological Supply Company, North Carolina, USA.

The toxic fragments encoded by the hybrid gene products are tested for activity towards three different insect species as described above. *M. sexta* is susceptible to both CryIC and CryIE. As may be anticipated from their sensitivity to trypsin, hybrids F59 and F71 are not active against this insect (Table 1). Although H7 is converted by trypsin to stable 65 kDa proteins, it is not toxic to *M. sexta*. All of the other hybrids given in Table 1 are toxic and are apparently in the native, biologically active conformation.

The 65 kDa fragment of CryIC is highly toxic towards *S. exigua* and *M. brassicae,* whereas CryIE is not. G27 (Table 1; Figure 2), a CryIE-CryIC hybrid with a crossover at the junction of domain II and III is active towards both insects. This demonstrates that domain III of CryIC confers full activity towards *S. exigua* and *M. brassicae*. Hybrid H8, which differs in only three amino acid residues (see Figure 3) from G27, although active against *M. sexta*, is not active against *S. exigua* and *M. brassicae*.

F26 (Table 1; Figure 3), the reciprocal hybrid of G27, in which domain III of CryIC has been exchanged by domain III of CryIE, is not active against *S. exigua* or *M. brassicae*. Apparently, although the protein is toxic to *M. sexta*, the CryIC sequences running from amino acid

28-462 are not sufficient to kill *S. exigua* and *M. brassicae*. Only when CryIC sequences up to amino acid residue 602 are present in the hybrid (E7) is insecticidal activity against these insects restored.

The present disclosure indicates that amino acid residues from 478-602 of CryIC can confer high insecticidal activity to CryIE against *S. exigua* and *M. brassicae*.

Biotinylation Of Crystal Proteins And Binding Assays

Biotinylation is performed using biotin-N-hydroxysuccinimide ester essentially as described by the manufacturer (Amersham). 1 mg of crystal protein is incubated with 40 ml biotinylation reagent in 50 mM $NaHCO_3$, 150 mM NaCl, pH8, for one hour at 20°C. The solution is loaded on a Sephadex 25 column equilibrated with the same buffer containing 0.1% BSA to remove unbound biotin, and samples of the fractions are spotted on a nitrocellulose membrane. Fractions containing biotinylated crystal proteins are visualized using streptavidine-peroxidase conjugate (Amersham) which catalyzes the oxidation of luminol, resulting in chemiluminescence (ECL, Amersham), and pooled.

Brush border membrane vesicles are isolated as described by Wolfersberger *et al.* (1987) (Comp. Biochem. Physiol. 86a, pp. 301-308) except that the vesicles are washed once more with isolation buffer containing 0.1% Tween 20. Binding of biotinylated crystal proteins to brush border membrane vesicles (100 mg/ml) is performed in 100 ml of PBS containing 1% BSA, 0.1% Tween-20 (pH 7.6). Vesicles (20 µg vesicle protein) are incubated with 10 ng biotinylated crystal proteins in the presence or absence of 1000-fold excess of unlabelled crystal proteins for 1 hour at 20°C. Subsequently, the vesicles are re-isolated by centrifugation for 10 minutes at 14,000 g in an Eppendorf centrifuge, washed twice with binding buffer, re-suspended in sample buffer, denatured by heating, and loaded on 7.5% polyacrylamide gels. After electrophoresis, proteins are blotted to nitrocellulose membranes and biotinylated crystal proteins that are re-isolated with the vesicles are visualized by incubation of the nitrocellulose with streptavidin-peroxidase conjugate (Amersham), which catalyzes the oxidation of luminol, resulting in chemiluminescence (ECL, Amersham).

Because binding to epithelial gut cells is a key step in the mode of action of crystal proteins, the binding of crystal proteins to *S. exigua* brush border membrane vesicles is investigated in heterologous competition experiments. Competition experiments demonstrate that the binding of labeled CryIC (Figure 4A, lane a) and labeled F26 (not shown) can be outcompeted by an excess of both unlabelled CryIC (lane b) or F26 (lane e) but not with an excess of G27 (lane c) or CryIE (lane d). Furthermore, binding of labeled G27 (Figure 4B, lane a) and labeled CryIE (not shown) can be outcompeted by an excess of G27 (lane b) or CryIE (lane d), but not with an excess of CryIC (lane a) or F26 (lane e). From these results, it is concluded that G27 and CryIE recognize the same binding sites on *S. exigua* midgut membranes and that these sites differ from those that are recognized by CryIC and F26. The toxicity and binding assays combined demonstrate that G27 is as toxic as CryIC but that it binds a receptor different therefrom. As insects can develop resistance against a crystal protein by changing receptor binding characteristics, G27 may be used in resistance management programs as an alternative to CryIC.

Expression of *cryIE/cryIC* Hybrid Toxin Genes In Heterologous Systems

The G27 *cryIE/cryIC* hybrid toxin gene is expressed in *E.coli,* and the gene product exhibits at least the same insecticidal activity (at least against *Spodoptera)* as CryIC. Moreover, the product exhibits an increase in such activity when expressed in a *Bacillus thuringiensis* strain (see below). The gene encoding the G27 hybrid toxin is introduced into a suitable shuttle vector system, which is then introduced into an appropriate B.t. host. Such transformed cells are then cultured, and the resulting toxin from both whole cultures and purified crystals is assayed for insecticidal activity.

Construction Of A G27-Containing Shuttle Vector, Transformation Of Bt51, And Purification Of Toxin Protein Therefrom

The gene encoding hybrid G27 (3.4 kb) is cleaved from a pKK233 *E. coli* expression plasmid using *Nco*I and *Xho*I. The *Xho*I site is filled in using the Klenow fragment of *E. coli* DNA Polymerase I. The resulting fragment is ligated to *NcoI/Sma*I-digested pSB635 (pBluescriptKS+, P_{cryIC}, and the CryIA(c) transcription terminator). The resulting plasmid, pSB453, is digested with *Apa*I and *Not*I, yielding a 4.2 kbp fragment carrying the promoter, the hybrid G27 ORF, and the terminator. This fragment is ligated to *Apa*I/*Not*I-digested pSB634 (shuttle vector containing

pBC16.1 and pBluescriptKS+), yielding pSB456 (see Figure 5). Plasmid DNA isolated from *E. coli* DH10B is used to transform the crystal toxin minus B.t. strain, Bt51. Positive isolates are tetracycline resistant, show the presence of pSB456, and contain large inclusions corresponding to a 135 kDa protein (as determined by SDS-PAGE). G27 hybrid toxin samples are prepared from cultures of transformed Bt51 grown through sporulation at 30°C in CYS-Tc[10] media. Insecticidal bioassays (Table 2) are performed on both full whole cultures and on washed crystal protein preparations. Controls include Bt51 (pSB440) containing the CryIC toxin and Bt51 (pSB636) containing CryIE. Toxin concentrations are estimated by SDS-PAGE.

TABLE 2

Toxin	LC_{50}				
	Whole Culture (ppt)			Washed Crystal Protein (ppm)	
CrylC	56(2)	36(2)	40(4)	7.8(2)	8.1(4)
CrylE	79(1)	78(1)	33(4)	11.1(6)	7.5(4)
G27	29(2)	21(2)	25(4)	4.7(4)	6.0(4)
Ratio (IC/G27)	1.93	1.71	1.60	1.66	1.35

Table 2. Bioassay of the hybrid toxin G27 in comparison to CryIC and CryIE. The number of samples is given in parentheses. The hybrid toxin G27 is about 50% more effective than either CryIE or CryIC with respect to toxicity to *Spodoptera sp.*

Production And Selection Of Cry1G/Cry1C Hybrid Toxins

To obtain Cry1G/Cry1C hybrid toxins by *in vivo* recombination, expression vector pHK26 was constructed with a C-terminal truncated *cryIG* (a.k.a. Cry9A) gene (*see,* SEQ ID NO:9) and a N-terminal truncated *cryIC* gene (*see,* SEQ ID NO:1) cloned in tandem. The plasmid pHK26 contains the *trc* promoter followed by bases 1-1650 of *cryIG*, part of the pBluescript SK+ polylinker, and bases 266-3570 of *cryIC*. pHK26 is a derivative of pRM7 in which the cry1A(b) coding sequences from *Nco*I to *Bgl*II have been replaced by part of the *cry1G* gene. The 1650 bp *Nco*I-*Bgl*II *cry1G* fragment was isolated by PCR amplification from plasmid pSB1501 using the primers dGCTAGCCATGGATCAAAATAAACACGGAATTATTG (SEQ ID NO:14) and dCTGGTCAGATCTTTGAAGTAGAGCTCC (SEQ ID NO:15). After allowing

intramolecular recombination of pHK26 in *E. coli* strain JM101, plasmid DNA was isolated and digested with *Bam*HI and *Pin*AI to linearize non-recombinant plasmids. Both *Bam*HI as well as *Pin*AI have unique recognition sites in pHK26, in the polylinker and at position 1074 of *cryIC*, respectively. The overlap between the two truncated *cry* genes in pHK26 that allows recombination extends approximately 1400 base pairs, yet primary interest was in recombinations in or close to domain III. Therefore, *Pin*AI was chosen rather than a second enzyme with a recognition site in the polylinker. This strategy allowed linearization of recombinants with crossovers in front of the *Pin*AI site, thereby effectively selecting for recombinants with crossovers in or near the domain III-encoding sequences.

Digested plasmids were transferred to *E. coli* XL1 cells by transformation, and plasmids from transformants were subsequently analyzed by restriction enzyme digestion and DNA electrophoresis. Over 80% of the transformants contained a plasmid with an insert size corresponding to a single, intact *cry* gene, indicating that selection for homologous recombination events had been efficient. Thirty separate colonies were grown in TB medium and assayed for production of alkaline-soluble protoxins that could be converted to stable 65 kD toxic fragments upon trypsin incubation. This screening method yielded 6 colonies producing a stable 65 kD toxic fragment of the expected size. The location of the crossovers in the hybrid genes was first determined by restriction analysis and finally by nucleotide sequencing. Only three different crossover sites occurred in the 6 hybrid genes thus tested. The hybrid genes were designated HK28-12, HK28-1, and HK28-24. The location of the three different crossover sites is shown in Figures 6A and 6B. The three crossovers are located close to the border between domains II and III, with the three hybrid toxins, designated HK28-12, HK28-1, and HK28-24, differing only one amino acid from each other. Both the solubility of the hybrid protoxins as well as the occurrence of trypsin-resistant products of the expected size suggested that these hybrids proteins were properly folded and might have biological activity. This was subsequently tested against larvae of *Spodoptera exigua*.

Toxicity of CryIG/CryIC Hybrid Toxins Towards *Spodoptera exigua*

The *cryIC*, *cryIG*, and newly isolated *cryIG/cryIC* hybrid genes were introduced in *E. coli* strain XL1-blue and grown for 48 hours at 28°C in TB medium with ampicillin. Cells were disrupted by sonification, and protoxin-containing crystals were isolated by cetrifugation. After washing the crystals, the protoxins were solubilized at high pH and the concentration of the 140 kD protoxins in the supernatant was estimated by SDS-PAGE. These samples were assayed for their toxicity to *S. exigua* larvae. Results are shown in Figure 7.

CryIG protoxin is much less toxic to *S. exigua* than CryIC. The hybrids containing domain III of CryIC are significantly more toxic than Cry1G. These results show that, as was demonstrated earlier for CryIE and Cry1A(b), Cry1G can be made considerably more toxic to *S. exigua* by substituting its domain III with that of CryIC. For example, hybrid HK28-24 (SEQ ID NO:12) is much more toxic to *S. exigua* than Cry1G (SEQ ID NO:10). Hybrid HK28-24 is also much more toxic to *S. frugiperda* than Cry1G (data not shown).

Although the present invention has been particularly described with reference to the production of Cry1E/Cry1C and Cry1G/Cry1C hybrid toxins, the routineer in the art will appreciate that many other hybrid toxins having improved insecticidal characteristics may be produced according to the present disclosure. SEQ ID NOs:7 and 8, for example, depict the nucleotide and amino acid sequences, respectively, of a CryIA/CryIC hybrid toxin fragment according to the invention that has improved insecticidal activity. Hybrid toxins may be produced comprising domain III of CryIC and the N-terminal region, including domains I and II, of any other Cry protein. In terms of bioassays, the hybrid toxin-carrying transformants may be grown in SOP media to expedite the assay procedures and reduce the volumes of material required. Moreover, the genes encoding the Cry1E/Cry1C, Cry1G/Cry1C, Cry1A/Cry1C, and/or other hybrid toxins according to the invention may be transferred into toxin-encoding strains of B.t. and/or integrated into the chromosome of selected strains of B.t. or introduced into plant genomes to provide for insecticidal activity *in situ* within the plant *per se*. In this regard, it is particularly preferred that the recombinant DNA encoding the toxins is modified so that codons that are preferred by the plant into which the recombinant DNA is to be inserted are used, whereby expression of the thus

modified DNA in the plant yields substantially similar protein to that obtained by expression of the unmodified recombinant DNA in the organism in which the protein components of the hybrid toxin or toxin fragments are endogenous.

Isolation of Additional B.t. Toxin Genes Based on Sequence Similarity to Known B.t. Toxin Genes

A library is plated at a density of approximately 8,000 pfu per 10 cm Petri dish, and filter lifts of the plaques are made after 7 hours growth at 37°C. The plaque lifts are probed with the cDNA set forth in SEQ ID NO:1, 3, or 9 labeled with 32P-dCTP by the random priming method by means of a PrimeTime kit (International Biotechnologies, Inc., New Haven, CT). Exemplary hybridization conditions are 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C. After hybridization overnight, the filters are washed with 2X SSC, 1% SDS at 50°C. Positively hybridizing plaques are detected by autoradiography. After purification to single plaques, cDNA inserts are isolated, and their sequences determined by the chain termination method using dideoxy terminators labeled with fluorescent dyes (Applied Biosystems, Inc., Foster City, CA). This experimental protocol can be used by one of ordinary skill in the art to obtain B.t. toxin genes substantially similar to those set forth in the Sequence Listing.

What Is Claimed Is:

1. An isolated *Bacillus thuringiensis* hybrid toxin fragment, comprising:

a) at a C-terminus of said fragment, domain III of a first Cry protein; and

b) at an N-terminus of said fragment, an N-terminal region of a second Cry protein.

2. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said first Cry protein is CryIC.

3. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said second Cry protein is selected from the group consisting of CryIA, CryIE, and CryIG.

4. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 3, wherein said second Cry protein is CryIA.

5. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 3, wherein said second Cry protein is CryIE.

6. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 3, wherein said second Cry protein is CryIG.

7. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said first Cry protein is CryIC, and wherein said second Cry protein is CryIA, CryIE, or CryIG.

8. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said N-terminal region of said second Cry protein comprises domain II of said second Cry protein.

9. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said N-terminal region of said second Cry protein comprises domains I and II of said second Cry protein.

10. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said C-terminus comprises the sequence from amino acid position 454 to position 602 of Cry IC, or a

sequence substantially similar to said sequence from amino acid position 454 to position 602 of Cry IC.

11. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 10, wherein said C-terminus comprises the sequence from amino acid position 454 to position 602 of SEQ ID NO:2, or a sequence substantially similar to said sequence from amino acid position 454 to position 602 of SEQ ID NO:2.

12. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said C-terminus comprises the sequence from amino acid position 478 to 602 of Cry IC, or a sequence substantially similar to said sequence from amino acid position 478 to 602 of Cry IC.

13. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 12, wherein said C-terminus comprises the sequence from amino acid position 478 to position 602 of SEQ ID NO:2, or a sequence substantially similar to said sequence from amino acid position 478 to position 602 of SEQ ID NO:2.

14. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, comprising a sequence selected from the group consisting of:

a) amino acids 1-620 of SEQ ID NO:6;

b) amino acids 1-620 of SEQ ID NO:6, wherein at least one of the following substitutions is present:

Ile at position 609 is replaced with Leu,

Ala at position 618 is replaced with Glu,

Ser at position 620 is replaced with Tyr; and

c) a sequence substantially similar to amino acids 1-620 of SEQ ID NO:6.

15. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, comprising a sequence selected from the group consisting of:

a) amino acids 1-627 of SEQ ID NO:8;

b) amino acids 1-627 of SEQ ID NO:8, wherein at least one of the following substitutions is present:

Ile at position 617 is replaced with Leu,

Ala at position 625 is replaced with Glu,

Ser at position 627 is replaced with Tyr; and

c) a sequence substantially similar to amino acids 1-627 of SEQ ID NO:8.

16. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, comprising a sequence selected from the group consisting of:

a) amino acids 1-602 of SEQ ID NO:12; and

b) a sequence substantially similar to amino acids 1-602 of SEQ ID NO:12.

17. An isolated DNA molecule encoding a protein that comprises the amino acid sequence of the hybrid toxin fragment of claim 1.

18. An isolated DNA molecule encoding a protein that comprises the amino acid sequence of the hybrid toxin fragment of claim 14.

19. An isolated DNA molecule encoding a protein that comprises the amino acid sequence of the hybrid toxin fragment of claim 15.

20. An isolated DNA molecule encoding a protein that comprises the amino acid sequence of the hybrid toxin fragment of claim 16.

21. An isolated *Bacillus thuringiensis* hybrid toxin fragment according to claim 1, wherein said hybrid toxin fragment binds to a binding site in an insect gut that is different than the site bound by said first Cry protein.

22. An isolated DNA molecule according to claim 17, which further encodes a protein having at least one of the following properties: herbicide resistance, plant growth-promoting, anti-fungal, anti-bacterial, anti-viral, and anti-nematode properties.

23. An isolated DNA molecule according to claim 17, which is modified to optimize expression in a heterologous host, said modifications selected from the group consisting of codon optimization for the intended host and removal of known mRNA instability motifs or polyadenylation signals.

24. An isolated DNA molecule that is complementary to the DNA molecule of claim 17.

25. A recombinant vector comprising the DNA molecule of claim 17.

26. An isolated cell transformed with the DNA molecule of claim 17.

27. A plant transformed with the DNA molecule of claim 17, wherein the progeny of such plant contains the DNA molecule stably incorporated and heritable in a Mendelian manner.

28. Seeds of the plant of claim 27.

29. Protein derived from expression of the DNA molecule of claim 17.

30. An insecticidal composition comprising the hybrid toxin fragment of claim 1.

31. A process for controlling insects, comprising exposing them to the insecticidal composition of claim 30.

32. A method of producing a protein, comprising expressing the DNA molecule of claim 17.

33. An insecticidal composition comprising the isolated cell of claim 26.

34. A process for controlling insects, comprising exposing them to the insecticidal composition of claim 33.

35. An isolated *Bacillus thuringiensis* hybrid toxin fragment, comprising amino acids 1-602 of SEQ ID NO:12.

36. An isolated *Bacillus thuringiensis* hybrid toxin fragment that has at least 95% sequence identity with, and has substantially the same insecticidal specificity and substantially the same insecticidal activity as the hybrid toxin fragment of claim 35.

37. An isolated DNA molecule encoding a protein that comprises the sequence of the hybrid toxin fragment of claim 35.

38. An isolated DNA molecule encoding a protein that comprises the sequence of the hybrid toxin fragment of claim 36.

39. An isolated DNA molecule that comprises the sequence of nucleotides 1-1806 of SEQ ID NO:11.

40. An isolated DNA molecule that hybridizes to the DNA molecule of claim 39 under the following set of conditions: hybridization at 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C; wash with 2X SSC, 1% SDS, at 50°C.

ABSTRACT

The present invention provides, *inter alia,* a B.t. hybrid toxin fragment comprising at its C-terminus domain III of a first Cry protein, or a part of said domain or a protein substantially similar to said domain; and comprising at its N-terminus the N-terminal region of a second Cry protein, or a part of said region or a protein substantially similar to said region.

FIG. 1

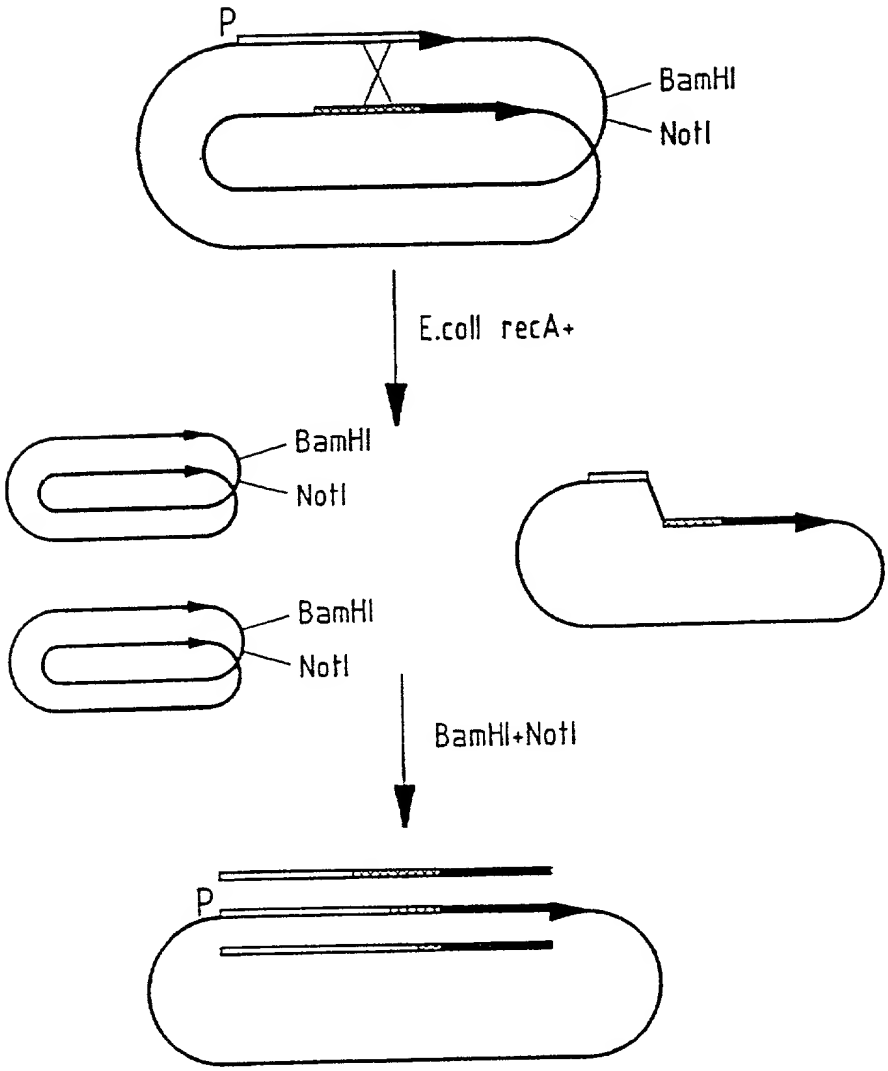


FIG. 2

CryIE-CryIC HYBRIDS

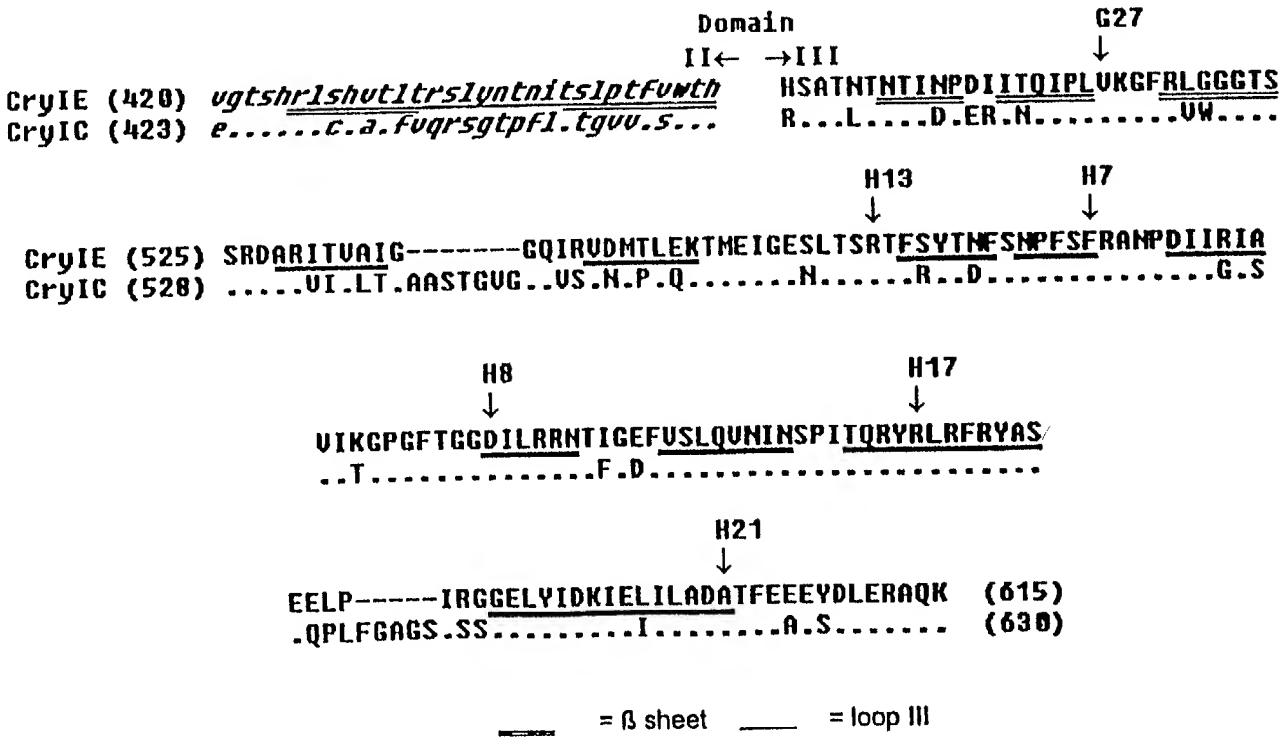


FIG. 3

CryIC-CryIE HYBRIDS

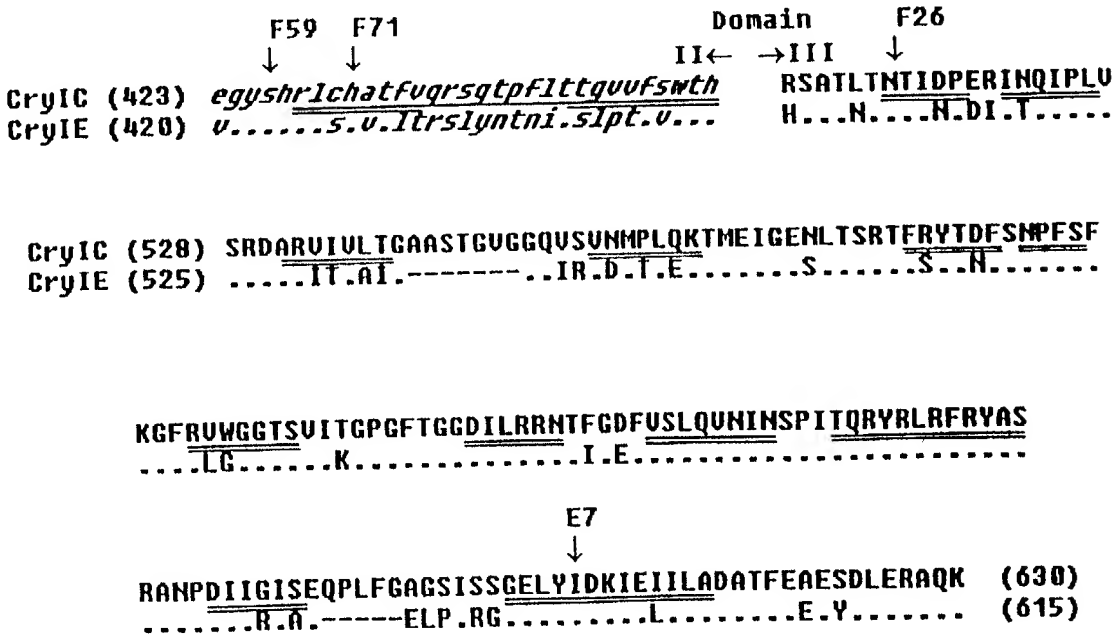
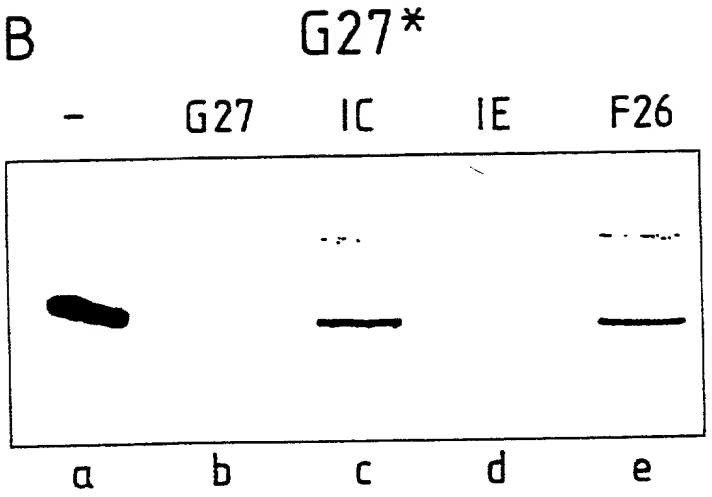


FIG. 4



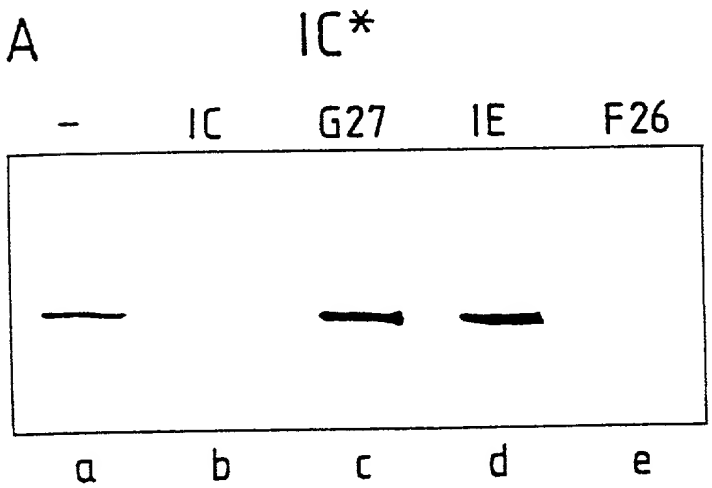
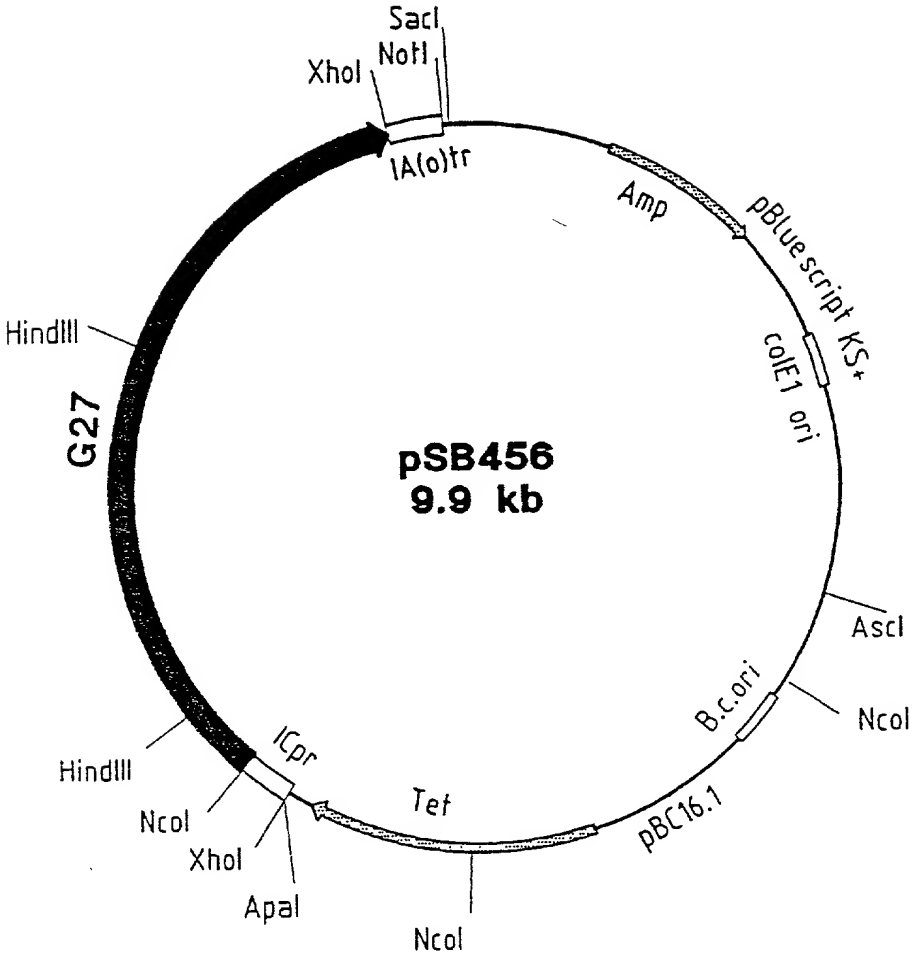


FIG. 5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colE1 ori
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B.c.ori
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XhoI
NcoI
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ICpr
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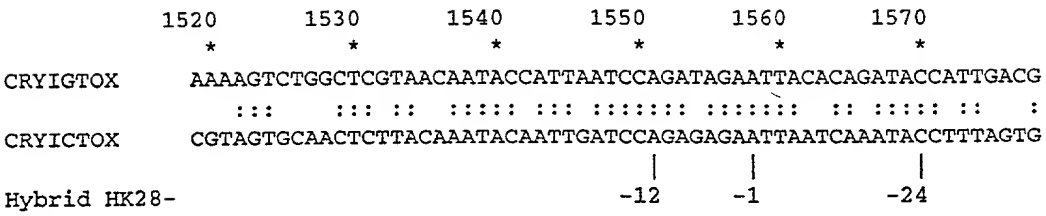
9.9 kb

FIG. 6A


1520
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1560
1570
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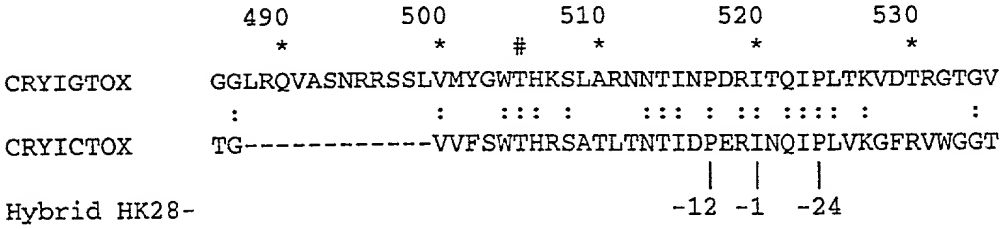
Hybrid HK28-
-12
-1
-24

FIG. 6B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530
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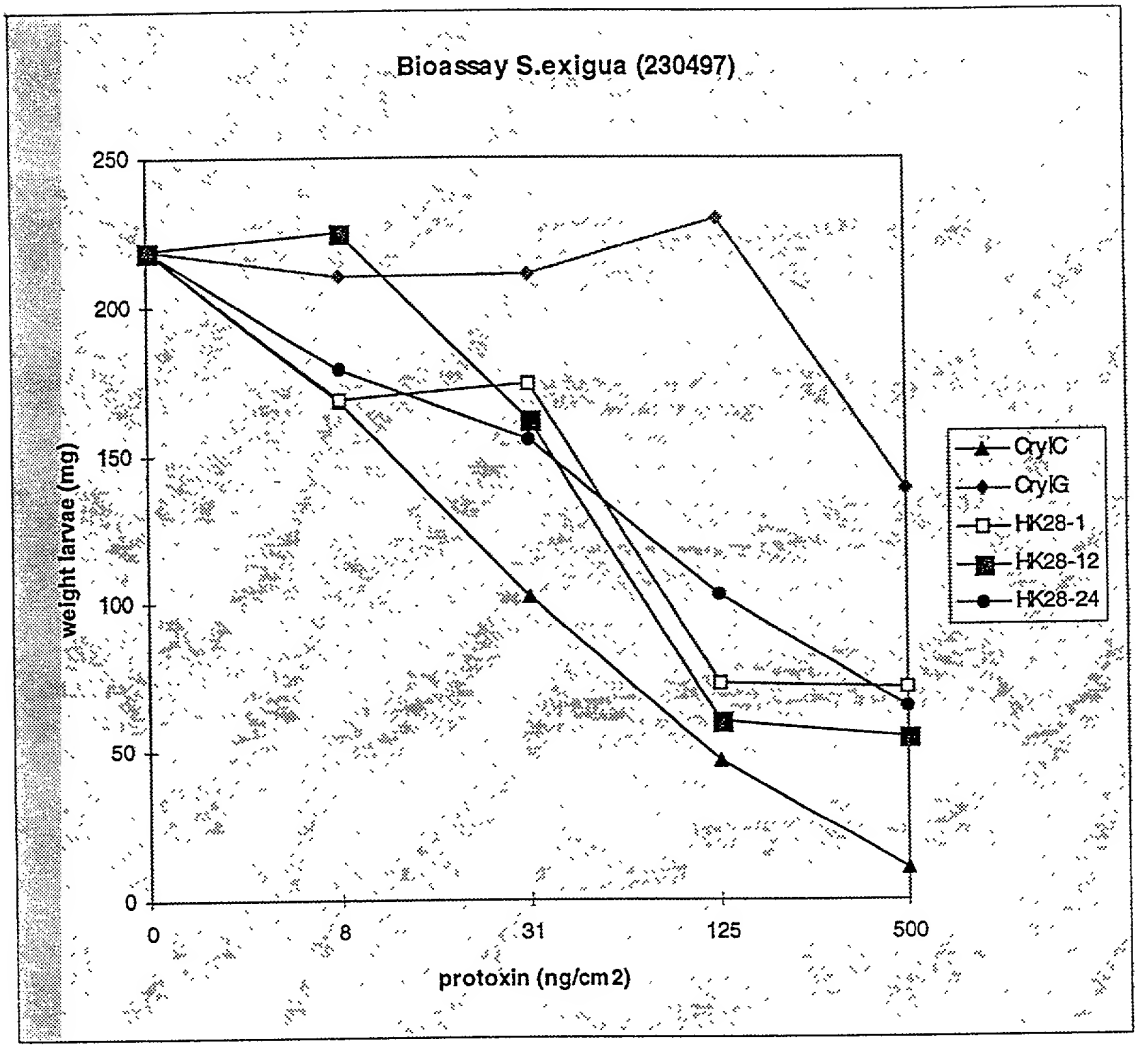
CRYICTOX TG----------VVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGT
Hybrid HK28-
-12 -1 -24

FIG. 7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weight larvae (mg)
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200
150
100
50
0
0
8
31
125
500
protoxin (ng/cm2)
CryIC
CryIG
HK28-1
HK28-12
HK28-24

DECLARATION AND POWER OF ATTORNEY FOR U.S. PATENT APPLICATIONS

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe I am an original, first and joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled

Hybrid Toxin

the specification of which was filed on December 31, 1997 as U.S. Application No. **09/001,982.**

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims.

I acknowledge my duty to disclose all information which is known by me to be material to the patentability of this application as defined in 37 C.F.R. §1.56.

I hereby claim the benefit under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate listed below and under 35 U.S.C. §365(a) of any PCT international application(s) designating at least one country other than the United States listed below and have also listed below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application the priority of which is claimed for that subject matter:

Country, Region or PCT	Application No.	Filing Date	Priority Claimed
Great Britain	9318207.9	September 2, 1993	Yes

I hereby claim the benefit under 35 USC §119(e) of any United States provisional application(s) listed below:

None

I hereby claim the benefit under 35 U.S.C. §120 of any United States application(s) listed below and under 35 U.S.C. §365(c) of any PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of 35 U.S.C. §112, I acknowledge the duty to disclose all information known by me to be material to patentability as defined in 37 C.F.R. §1.56 which became available between the filing date(s) of the prior application(s) and the national or PCT international filing date of this application:

United States Application No.	United States Filing or §371 Date	Status or U.S. Patent No.	International Application No.	International Filing Date
08/602,737	February 21, 1996	Pending	PCT/EP94/02909	September 1, 1994

I hereby appoint the attorneys and agents associated with Customer No. 001095, respectively and individually, as my attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith.

Please address all communications to J. Timothy Meigs, Novartis Corporation, Patent and Trademark Dept., P.O. Box 12257, Research Triangle Park, NC 27709-2257.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

FIRST JOINT INVENTOR:

Full name : **Hendrik Jan Bosch**

Signature : _____

Date : 04/09/98
(MM/DD/YY)

Citizenship : Netherlands

Residence : Oortlaan 20
NL-3572 ZM Utrecht
The Netherlands

SECOND JOINT INVENTOR:

Full name : **Willem Johannes Stiekema**

Signature : _____

Date : _____
(MM/DD/YY)

Citizenship : Netherlands

Residence : Leonard Roggeveenstraat 21
NL-6708 SL Wageningen
The Netherlands

IMPORTANT: Before this declaration is signed, the patent application (the specification, the claims and this declaration) must be read and understood by each person signing it, and no changes may be made in the application after this declaration has been signed.

Case 130-4080/PCT/CIP

DECLARATION AND POWER OF ATTORNEY FOR U.S. PATENT APPLICATIONS

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe I am an original, first and joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled

Hybrid Toxin

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Country, Region or PCT	Application No.	Filing Date	Priority Claimed
Great Britain	9318207.9	September 2, 1993	Yes

I hereby claim the benefit under 35 USC §119(e) of any United States provisional application(s) listed below:

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United States Application No.	United States Filing or §371 Date	Status or U.S. Patent No.	International Application No.	International Filing Date
08/602,737	February 21, 1996	Pending	PCT/EP94/02909	September 1, 1994

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FIRST JOINT INVENTOR:

Full name : **Hendrik Jan Bosch**

Signature : _____

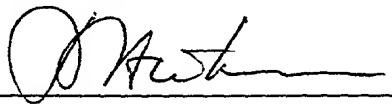
Date : _____
(MM/DD/YY)

Citizenship : Netherlands

Residence : Oortlaan 20
NL-3572 ZM Utrecht
The Netherlands

SECOND JOINT INVENTOR:

Full name : **Willem Johannes Stiekema**

Signature : 

Date : 04/08/98
(MM/DD/YY)

Citizenship : Netherlands

Residence : Leonard Roggeveenstraat 21
NL-6708 SL Wageningen
The Netherlands

IMPORTANT: Before this declaration is signed, the patent application (the specification, the claims and this declaration) must be read and understood by each person signing it, and no changes may be made in the application after this declaration has been signed.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bosch, Hendrick J.
Stiekema, Willem J.

(ii) TITLE OF INVENTION: Hybrid Toxin

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Novartis Corporation
(B) STREET: 3054 Cornwallis Road
(C) CITY: Research Triangle Park
(D) STATE: NC
(E) COUNTRY: USA
(F) ZIP: 27709

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/602,737
(B) FILING DATE: 21-FEB-1996

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Meigs, J. Timothy
(B) REGISTRATION NUMBER: 38,241
(C) REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 919-541-8587
(B) TELEFAX: 919-541-8689

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bacillus thuringiensis

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT        48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1               5                  10                  15

AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT        96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
            20                  25                  30

TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC       144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
        35                  40                  45

TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG       192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
    50                  55                  60

GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA       240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65                  70                  75                  80

CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT       288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
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GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA       336
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
            100                 105                 110

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Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Glu Thr Arg Thr Arg
        115                 120                 125

GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT       432
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
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GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT      528
Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
                165                 170                 175

TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT      576
Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
            180                 185                 190

AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT      624
Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
        195                 200                 205

ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT      672
Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
    210                 215                 220

TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA      720
Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225                 230                 235                 240

GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT      768
Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
                245                 250                 255

CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT      816
Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
            260                 265                 270

AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC      864
Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
        275                 280                 285

GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG      912
Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
    290                 295                 300

AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT      960
Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
305                 310                 315                 320

TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC     1008
Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
                325                 330                 335

ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA     1056
Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
            340                 345                 350

TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT     1104
Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
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        355                 360                 365

TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT      1152
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    370                 375                 380

GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT      1200
Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
385                 390                 395                 400

CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT      1248
Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
                405                 410                 415

AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA      1296
Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
            420                 425                 430

ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA      1344
Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
        435                 440                 445

TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA      1392
Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
    450                 455                 460

GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG      1440
Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
465                 470                 475                 480

GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT      1488
Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
                485                 490                 495

CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT      1536
Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
            500                 505                 510

TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT      1584
Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
        515                 520                 525

AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG      1632
Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
    530                 535                 540

GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA      1680
Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
545                 550                 555                 560

GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT      1728
Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
                565                 570                 575
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CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA      1776
Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
            580                 585                 590

CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT      1824
Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
        595                 600                 605

AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT      1872
Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
    610                 615                 620

TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT      1920
Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
625                 630                 635                 640

CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA      1968
Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
                645                 650                 655

TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG      2016
Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
            660                 665                 670

CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG      2064
Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
        675                 680                 685

CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA      2112
Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
    690                 695                 700

GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT      2160
Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
705                 710                 715                 720

GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG      2208
Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
                725                 730                 735

TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA      2256
Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
            740                 745                 750

GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC      2304
Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
        755                 760                 765

TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT      2352
Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
    770                 775                 780
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GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC      2400
Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
785                 790                 795                 800

GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT      2448
Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
                805                 810                 815

CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT      2496
Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
            820                 825                 830

TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT      2544
Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
        835                 840                 845

GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC      2592
Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
    850                 855                 860

CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA      2640
His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
865                 870                 875                 880

GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC      2688
Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
                885                 890                 895

AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA      2736
Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
            900                 905                 910

AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA      2784
Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
        915                 920                 925

CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT      2832
Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
    930                 935                 940

CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT      2880
His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
945                 950                 955                 960

GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG      2928
Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
                965                 970                 975

TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT      2976
Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
            980                 985                 990

AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG      3024
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Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
        995                 1000                1005

CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA      3072
Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
    1010                1015                1020

GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT      3120
Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1025                1030                1035                1040

GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT      3168
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
                1045                1050                1055

GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA      3216
Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
            1060                1065                1070

GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG      3264
Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
        1075                1080                1085

ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT      3312
Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
    1090                1095                1100

GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA      3360
Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
1105                1110                1115                1120

GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT      3408
Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
                1125                1130                1135

GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT      3456
Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
            1140                1145                1150

GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT      3504
Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
        1155                1160                1165

GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA      3552
Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
    1170                1175                1180

CTC CTT ATG GAG GAA                                                 3567
Leu Leu Met Glu Glu
1185
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1               5                  10                  15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
            20                  25                  30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
        35                  40                  45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
    50                  55                  60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65                  70                  75                  80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
                85                  90                  95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
            100                 105                 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Glu Thr Arg Thr Arg
        115                 120                 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
    130                 135                 140

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145                 150                 155                 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
                165                 170                 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
            180                 185                 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
        195                 200                 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
    210                 215                 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
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225 230 235 240

Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
245 250 255

Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
260 265 270

Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
275 280 285

Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
290 295 300

Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
305 310 315 320

Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
325 330 335

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
340 345 350

Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
355 360 365

Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
370 375 380

Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
385 390 395 400

Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
435 440 445

Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
450 455 460

Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
485 490 495

Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
500 505 510

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Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
        515                 520                 525

Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
    530                 535                 540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
545                 550                 555                 560

Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
                565                 570                 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
            580                 585                 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
        595                 600                 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
    610                 615                 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
625                 630                 635                 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
                645                 650                 655

Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
            660                 665                 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
        675                 680                 685

Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
    690                 695                 700

Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
705                 710                 715                 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
                725                 730                 735

Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
            740                 745                 750

Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
        755                 760                 765

Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
    770                 775                 780

Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
785                 790                 795                 800
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Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
805 810 815

Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
835 840 845

Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
900 905 910

Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
915 920 925

Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
930 935 940

His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
965 970 975

Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
980 985 990

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
995 1000 1005

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
1010 1015 1020

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1025 1030 1035 1040

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
1045 1050 1055

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
1060 1065 1070

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly

1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1170 1175 1180

Leu Leu Met Glu Glu
1185

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bacillus thuringiensis

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GAG ATA GTG AAT AAT CAG AAT CAA TGC GTG CCT TAT AAT TGT TTA 48
Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
1 5 10 15

AAT AAT CCT GAA AAT GAG ATA TTA GAT ATT GAA AGG TCA AAT AGT ACT 96
Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr

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                20                  25                  30

GTA GCA ACA AAC ATC GCC TTG GAG ATT AGT CGT CTG CTC GCT TCC GCA      144
Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala
        35                  40                  45

ACT CCA ATA GGG GGG ATT TTA TTA GGA TTG TTT GAT GCA ATA TGG GGG      192
Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly
    50                  55                  60

TCT ATA GGC CCT TCA CAA TGG GAT TTA TTT TTA GAG CAA ATT GAG CTA      240
Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu
65                  70                  75                  80

TTG ATT GAC CAA AAA ATA GAG GAA TTC GCT AGA AAC CAG GCA ATT TCT      288
Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser
                85                  90                  95

AGA TTG GAA GGG ATA AGC AGT CTG TAC GGA ATT TAT ACA GAA GCT TTT      336
Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe
            100                 105                 110

AGA GAG TGG GAA GCA GAT CCT ACT AAT CCA GCA TTA AAA GAA GAG ATG      384
Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met
        115                 120                 125

CGT ACT CAA TTT AAT GAC ATG AAC AGT ATT CTT GTA ACA GCT ATT CCT      432
Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro
    130                 135                 140

CTT TTT TCA GTT CAA AAT TAT CAA GTC CCA TTT TTA TCA GTA TAT GTT      480
Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
145                 150                 155                 160

CAA GCT GCA AAT TTA CAT TTA TCG GTT TTG AGA GAT GTT TCA GTG TTT      528
Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
                165                 170                 175

GGG CAG GCT TGG GGA TTT GAT ATA GCA ACA ATA AAT AGT CGT TAT AAT      576
Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
            180                 185                 190

GAT CTG ACT AGA CTT ATT CCT ATA TAT ACA GAT TAT GCT GTA CGC TGG      624
Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
        195                 200                 205

TAC AAT ACG GGA TTA GAT CGC TTA CCA CGA ACT GGT GGG CTG CGA AAC      672
Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
    210                 215                 220

TGG GCA AGA TTT AAT CAG TTT AGA AGA GAG TTA ACA ATA TCA GTA TTA      720
Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
225                 230                 235                 240
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GAT ATT ATT TCT TTT TTC AGA AAT TAC GAT TCT AGA TTA TAT CCA ATT      768
Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
                245                 250                 255

CCA ACA AGC TCC CAA TTA ACG CGG GAA GTA TAT ACA GAT CCG GTA ATT      816
Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
            260                 265                 270

AAT ATA ACT GAC TAT AGA GTT GGC CCC AGC TTC GAG AAT ATT GAG AAC      864
Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
        275                 280                 285

TCA GCC ATT AGA AGC CCC CAC CTT ATG GAC TTC TTA AAT AAT TTG ACC      912
Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
    290                 295                 300

ATT GAT ACG GAT TTG ATT AGA GGT GTT CAC TAT TGG GCA GGG CAT CGT      960
Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
305                 310                 315                 320

GTA ACT TCT CAT TTT ACA GGT AGT TCT CAA GTG ATA ACA ACC CCT CAA     1008
Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
                325                 330                 335

TAT GGG ATA ACC GCA AAT GCG GAA CCA AGA CGA ACT ATT GCT CCT AGT     1056
Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
            340                 345                 350

ACT TTT CCA GGT CTT AAC CTA TTT TAT AGA ACA TTA TCA AAT CCT TTC     1104
Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
        355                 360                 365

TTC CGA AGA TCA GAA AAT ATT ACT CCT ACC TTA GGG ATA AAT GTA GTA     1152
Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
    370                 375                 380

CAG GGA GTA GGG TTC ATT CAA CCA AAT AAT GCT GAA GTT CTA TAT AGA     1200
Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
385                 390                 395                 400

AGT AGG GGG ACA GTA GAT TCT CTT AAT GAG TTA CCA ATT GAT GGT GAG     1248
Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
                405                 410                 415

AAT TCA TTA GTT GGA TAT AGT CAT CGA TTA AGT CAT GTT ACA CTA ACC     1296
Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
            420                 425                 430

AGG TCG TTA TAT AAT ACT AAT ATA ACT AGC CTG CCA ACA TTT GTT TGG     1344
Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
        435                 440                 445
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ACA CAT CAC AGT GCT ACT AAT ACA AAT ACA ATT AAT CCA GAT ATT ATT      1392
Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
    450                 455                 460

ACA CAA ATA CCT TTA GTG AAA GGA TTT AGA CTT GGT GGT GGC ACC TCT      1440
Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Leu Gly Gly Gly Thr Ser
465                 470                 475                 480

GTC ATT AAA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT CGA AGA AAT      1488
Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
                485                 490                 495

ACC ATT GGT GAG TTT GTG TCT TTA CAA GTC AAT ATT AAC TCA CCA ATT      1536
Thr Ile Gly Glu Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
            500                 505                 510

ACC CAA AGA TAC CGT TTA AGA TTT CGT TAT GCT TCC AGT AGG GAT GCA      1584
Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
        515                 520                 525

CGA ATT ACT GTA GCG ATA GGA GGA CAA ATT AGA GTA GAT ATG ACC CTT      1632
Arg Ile Thr Val Ala Ile Gly Gly Gln Ile Arg Val Asp Met Thr Leu
    530                 535                 540

GAA AAA ACC ATG GAA ATT GGG GAG AGC TTA ACA TCT AGA ACA TTT AGC      1680
Glu Lys Thr Met Glu Ile Gly Glu Ser Leu Thr Ser Arg Thr Phe Ser
545                 550                 555                 560

TAT ACC AAT TTT AGT AAT CCT TTT TCA TTT AGG GCT AAT CCA GAT ATA      1728
Tyr Thr Asn Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile
                565                 570                 575

ATT AGA ATA GCT GAA GAA CTT CCT ATT CGT GGT GGT GAG CTT TAT ATA      1776
Ile Arg Ile Ala Glu Glu Leu Pro Ile Arg Gly Gly Glu Leu Tyr Ile
            580                 585                 590

GAT AAA ATT GAA CTT ATT CTA GCA GAT GCA ACA TTT GAA GAA GAA TAT      1824
Asp Lys Ile Glu Leu Ile Leu Ala Asp Ala Thr Phe Glu Glu Glu Tyr
        595                 600                 605

GAT TTG GAA AGA GCA CAG AAG GCG GTG AAT GCC CTG TTT ACT TCT ACA      1872
Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr
    610                 615                 620

AAT CAA CTA GGG CTA AAA ACA GAT GTG ACG GAT TAT CAT ATT GAT CAA      1920
Asn Gln Leu Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
625                 630                 635                 640

GTT TCC AAT TTA GTT GAG TGT TTA TCG GAT GAA TTT TGT CTG GAT GAA      1968
Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
                645                 650                 655

AAG AGA GAA TTA TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT      2016
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Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
            660                 665                 670

GAA CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGG CAA       2064
Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln
        675                 680                 685

CCA GAC CGT GGC TGG AGA GGA AGC ACG GAT ATT ACT ATC CAA GGT GGA       2112
Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly
    690                 695                 700

GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA TTA CCG GGT ACC TTT GAT       2160
Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
705                 710                 715                 720

GAG TGC TAT CCA ACG TAT TTA TAT CAA AAA ATA GAT GAG TCG AAG TTA       2208
Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
                725                 730                 735

AAA GCT TAT ACC CGC TAT GAA TTA AGA GGG TAT ATC GAG GAT AGT CAA       2256
Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln
            740                 745                 750

GAC TTA GAA ATC TAT TTA ATT CGC TAC AAT GCA AAA CAC GAG ACA GTA       2304
Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
        755                 760                 765

AAC GTG CCA GGT ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA       2352
Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro
    770                 775                 780

ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG       2400
Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
785                 790                 795                 800

AAT CCT AAT CTA GAT TGC TCC TGC AGA GAC GGG GAA AAA TGT GCC CAT       2448
Asn Pro Asn Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
                805                 810                 815

CAT TCC CAT CAT TTC TCC TTG GAC ATT GAT GTT GGA TGT ACA GAC TTA       2496
His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
            820                 825                 830

AAT GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACA CAA GAT       2544
Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
        835                 840                 845

GGC TAT GCA AGA CTA GGA AAT CTA GAG TTT CTC GAA GAG AAC CCA CTA       2592
Gly Tyr Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Asn Pro Leu
    850                 855                 860

TTA GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAA AAA TGG AGA       2640
Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
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865                 870                 875                 880

GAC AAA TGC GAA AAA TTG GAA TGG GAA ACA AAT ATT GTT TAT AAA GAG      2688
Asp Lys Cys Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu
                885                 890                 895

GCA AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA      2736
Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg
            900                 905                 910

TTA CAA GCG GAT ACG AAT ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC      2784
Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
        915                 920                 925

GTT CAT AGC ATT CGA GAA GCG TAT CTG CCA GAG CTG TCT GTG ATT CCG      2832
Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro
    930                 935                 940

GGT GTC AAT GCG GCT ATT TTT GAA GAA TTA GAA GGG CGT ATT TTC ACT      2880
Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr
945                 950                 955                 960

GCA TTC TCC CTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC      2928
Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe
                965                 970                 975

AAT AAT GGC TTA TCA TGC TGG AAC GTG AAA GGG CAT GTA GAT GTA GAA      2976
Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
            980                 985                 990

GAA CAG AAC AAC CAT CGT TCG GTC CTT GTT GTT CCA GAA TGG GAA GCA      3024
Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
        995                 1000                1005

GAA GTG TCA CAA GAA GTT CGT GTT TGT CCG GGT CGT GGC TAT ATC CTT      3072
Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
    1010                1015                1020

CGT GTT ACA GCG TAC AAA GAG GGA TAT GGA GAG GGC TGT GTA ACG ATT      3120
Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
1025                1030                1035                1040

CAT GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA      3168
His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
                1045                1050                1055

GAA GAG GAA GTA TAT CCA AAC AAC ACG GTA ACG TGT AAT AAT TAT ACT      3216
Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr
            1060                1065                1070

GCG ACT CAA GAA GAA CAT GAG GGT ACG TAC ACT TCC CGT AAT CGA GGA      3264
Ala Thr Gln Glu Glu His Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
        1075                1080                1085
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TAT GAC GAA GCC TAT GAA AGC AAT TCT TCT GTA CAT GCG TCA GTC TAT      3312
Tyr Asp Glu Ala Tyr Glu Ser Asn Ser Ser Val His Ala Ser Val Tyr
    1090                1095                1100

GAA GAA AAA TCG TAT ACA GAT AGA CGA AGA GAG AAT CCT TGT GAA TCT      3360
Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu Ser
1105                1110                1115                1120

AAC AGA GGA TAT GGG GAT TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA      3408
Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
                1125                1130                1135

AAA GAA TTA GAG TAC TTC CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC      3456
Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
            1140                1145                1150

GGA GAA ACG GAA GGA ACA TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT      3504
Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
        1155                1160                1165

ATG GAG GAA                                                         3513
Met Glu Glu
    1170
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1171 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
  1               5                  10                  15

Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr
             20                  25                  30

Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala
         35                  40                  45

Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly
     50                  55                  60

Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu
 65                  70                  75                  80

Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser
```

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                85                  90                  95

Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe
            100                 105                 110

Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met
        115                 120                 125

Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro
    130                 135                 140

Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
145                 150                 155                 160

Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
                165                 170                 175

Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
            180                 185                 190

Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
        195                 200                 205

Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
    210                 215                 220

Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
225                 230                 235                 240

Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
                245                 250                 255

Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
            260                 265                 270

Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
        275                 280                 285

Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
    290                 295                 300

Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
305                 310                 315                 320

Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
                325                 330                 335

Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
            340                 345                 350

Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
        355                 360                 365
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Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
    370                 375                 380

Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
385                 390                 395                 400

Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
                405                 410                 415

Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
            420                 425                 430

Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
        435                 440                 445

Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
    450                 455                 460

Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Leu Gly Gly Gly Thr Ser
465                 470                 475                 480

Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
                485                 490                 495

Thr Ile Gly Glu Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
            500                 505                 510

Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
        515                 520                 525

Arg Ile Thr Val Ala Ile Gly Gly Gln Ile Arg Val Asp Met Thr Leu
    530                 535                 540

Glu Lys Thr Met Glu Ile Gly Glu Ser Leu Thr Ser Arg Thr Phe Ser
545                 550                 555                 560

Tyr Thr Asn Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile
                565                 570                 575

Ile Arg Ile Ala Glu Glu Leu Pro Ile Arg Gly Gly Glu Leu Tyr Ile
            580                 585                 590

Asp Lys Ile Glu Leu Ile Leu Ala Asp Ala Thr Phe Glu Glu Glu Tyr
        595                 600                 605

Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr
    610                 615                 620

Asn Gln Leu Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
625                 630                 635                 640

Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
                645                 650                 655
```

```
Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
            660                 665                 670

Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln
        675                 680                 685

Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly
    690                 695                 700

Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
705                 710                 715                 720

Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
                725                 730                 735

Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln
            740                 745                 750

Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
        755                 760                 765

Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro
    770                 775                 780

Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
785                 790                 795                 800

Asn Pro Asn Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
                805                 810                 815

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
            820                 825                 830

Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
        835                 840                 845

Gly Tyr Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Asn Pro Leu
    850                 855                 860

Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
865                 870                 875                 880

Asp Lys Cys Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu
                885                 890                 895

Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg
            900                 905                 910

Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
        915                 920                 925

Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro
```

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    930                 935                 940

Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr
945                 950                 955                 960

Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe
                965                 970                 975

Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
            980                 985                 990

Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
        995                 1000                1005

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
    1010                1015                1020

Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
1025                1030                1035                1040

His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
                1045                1050                1055

Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr
            1060                1065                1070

Ala Thr Gln Glu Glu His Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
        1075                1080                1085

Tyr Asp Glu Ala Tyr Glu Ser Asn Ser Ser Val His Ala Ser Val Tyr
    1090                1095                1100

Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu Ser
1105                1110                1115                1120

Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
                1125                1130                1135

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
            1140                1145                1150

Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
        1155                1160                1165

Met Glu Glu
    1170
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Hybrid sequence

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
ATG GAG ATA GTG AAT AAT CAG AAT CAA TGC GTG CCT TAT AAT TGT TTA        48
Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
 1               5                  10                  15

AAT AAT CCT GAA AAT GAG ATA TTA GAT ATT GAA AGG TCA AAT AGT ACT        96
Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr
            20                  25                  30

GTA GCA ACA AAC ATC GCC TTG GAG ATT AGT CGT CTG CTC GCT TCC GCA       144
Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala
        35                  40                  45

ACT CCA ATA GGG GGG ATT TTA TTA GGA TTG TTT GAT GCA ATA TGG GGG       192
Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly
    50                  55                  60

TCT ATA GGC CCT TCA CAA TGG GAT TTA TTT TTA GAG CAA ATT GAG CTA       240
Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu
65                  70                  75                  80

TTG ATT GAC CAA AAA ATA GAG GAA TTC GCT AGA AAC CAG GCA ATT TCT       288
Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser
                85                  90                  95

AGA TTG GAA GGG ATA AGC AGT CTG TAC GGA ATT TAT ACA GAA GCT TTT       336
Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe
            100                 105                 110

AGA GAG TGG GAA GCA GAT CCT ACT AAT CCA GCA TTA AAA GAA GAG ATG       384
Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met
        115                 120                 125

CGT ACT CAA TTT AAT GAC ATG AAC AGT ATT CTT GTA ACA GCT ATT CCT       432
Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro
    130                 135                 140
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CTT TTT TCA GTT CAA AAT TAT CAA GTC CCA TTT TTA TCA GTA TAT GTT        480
Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
145                 150                 155                 160

CAA GCT GCA AAT TTA CAT TTA TCG GTT TTG AGA GAT GTT TCA GTG TTT        528
Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
                165                 170                 175

GGG CAG GCT TGG GGA TTT GAT ATA GCA ACA ATA AAT AGT CGT TAT AAT        576
Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
            180                 185                 190

GAT CTG ACT AGA CTT ATT CCT ATA TAT ACA GAT TAT GCT GTA CGC TGG        624
Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
        195                 200                 205

TAC AAT ACG GGA TTA GAT CGC TTA CCA CGA ACT GGT GGG CTG CGA AAC        672
Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
    210                 215                 220

TGG GCA AGA TTT AAT CAG TTT AGA AGA GAG TTA ACA ATA TCA GTA TTA        720
Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
225                 230                 235                 240

GAT ATT ATT TCT TTT TTC AGA AAT TAC GAT TCT AGA TTA TAT CCA ATT        768
Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
                245                 250                 255

CCA ACA AGC TCC CAA TTA ACG CGG GAA GTA TAT ACA GAT CCG GTA ATT        816
Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
            260                 265                 270

AAT ATA ACT GAC TAT AGA GTT GGC CCC AGC TTC GAG AAT ATT GAG AAC        864
Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
        275                 280                 285

TCA GCC ATT AGA AGC CCC CAC CTT ATG GAC TTC TTA AAT AAT TTG ACC        912
Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
    290                 295                 300

ATT GAT ACG GAT TTG ATT AGA GGT GTT CAC TAT TGG GCA GGG CAT CGT        960
Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
305                 310                 315                 320

GTA ACT TCT CAT TTT ACA GGT AGT TCT CAA GTG ATA ACA ACC CCT CAA       1008
Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
                325                 330                 335

TAT GGG ATA ACC GCA AAT GCG GAA CCA AGA CGA ACT ATT GCT CCT AGT       1056
Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
            340                 345                 350
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ACT TTT CCA GGT CTT AAC CTA TTT TAT AGA ACA TTA TCA AAT CCT TTC      1104
Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
        355                 360                 365

TTC CGA AGA TCA GAA AAT ATT ACT CCT ACC TTA GGG ATA AAT GTA GTA      1152
Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
    370                 375                 380

CAG GGA GTA GGG TTC ATT CAA CCA AAT AAT GCT GAA GTT CTA TAT AGA      1200
Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
385                 390                 395                 400

AGT AGG GGG ACA GTA GAT TCT CTT AAT GAG TTA CCA ATT GAT GGT GAG      1248
Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
                405                 410                 415

AAT TCA TTA GTT GGA TAT AGT CAT CGA TTA AGT CAT GTT ACA CTA ACC      1296
Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
            420                 425                 430

AGG TCG TTA TAT AAT ACT AAT ATA ACT AGC CTG CCA ACA TTT GTT TGG      1344
Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
        435                 440                 445

ACA CAT CAC AGT GCT ACT AAT ACA AAT ACA ATT AAT CCA GAT ATT ATT      1392
Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
    450                 455                 460

ACA CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG GGC ACC TCT      1440
Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly Gly Thr Ser
465                 470                 475                 480

GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT CGA AGA AAT      1488
Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
                485                 490                 495

ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT TCA CCA ATT      1536
Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
            500                 505                 510

ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT AGG GAT GCA      1584
Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
        515                 520                 525

CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG GGA GGC CAA      1632
Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val Gly Gly Gln
    530                 535                 540

GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA GGG GAG AAC      1680
Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile Gly Glu Asn
545                 550                 555                 560

TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT CCT TTT TCA      1728
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Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn Pro Phe Ser
                565                 570                 575

TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA CCT CTA TTT      1776
Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln Pro Leu Phe
            580                 585                 590

GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT AAA ATT GAA      1824
Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp Lys Ile Glu
        595                 600                 605

ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT TTA GAA AGA      1872
Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg
    610                 615                 620

GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT CAA ATC GGG      1920
Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn Gln Ile Gly
625                 630                 635                 640

TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA TCC AAT TTA      1968
Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
                645                 650                 655

GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG CGA GAA TTG      2016
Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
            660                 665                 670

TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG CGG AAT TTA      2064
Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu
        675                 680                 685

CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA GAC CGT GGC      2112
Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly
    690                 695                 700

TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT GAC GTA TTC      2160
Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe
705                 710                 715                 720

AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG TGC TAT CCA      2208
Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro
                725                 730                 735

ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA GCT TAT ACC      2256
Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr
            740                 745                 750

CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC      2304
Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile
        755                 760                 765

TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT GTG CCA GGC      2352
Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly
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    770                 775                 780

ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC GGA AAG TGT      2400
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys
785                 790                 795                 800

GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT CCT GAT CTA      2448
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu
                805                 810                 815

GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT TCC CAT CAT      2496
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His
            820                 825                 830

TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC TTA      2544
Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu
        835                 840                 845

GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA AGA      2592
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg
    850                 855                 860

CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA GGG GAA GCA      2640
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala
865                 870                 875                 880

CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC AAA CGA GAG      2688
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu
                885                 890                 895

AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT      2736
Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser
            900                 905                 910

GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GTG GAT      2784
Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Val Asp
        915                 920                 925

ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT CAT AGA ATC      2832
Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile
    930                 935                 940

CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT GTC AAT GCG      2880
Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala
945                 950                 955                 960

GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG TAT TCC TTA      2928
Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser Leu
                965                 970                 975

TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT AAT GGC TTA      2976
Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu
            980                 985                 990
```

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TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG CAA AAC AAC      3024
Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn
        995                 1000                1005

CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA GTG TCA CAA      3072
His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln
    1010                1015                1020

GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT GTC ACA GCA      3120
Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
1025                1030                1035                1040

TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT GAG ATC GAA      3168
Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
                1045                1050                1055

GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA GAG GAA GTA      3216
Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val
            1060                1065                1070

TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG ACT CAA GAA      3264
Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly Thr Gln Glu
        1075                1080                1085

GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT GAC GAA GCC      3312
Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr Asp Glu Ala
    1090                1095                1100

TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA GTC TAT GAA      3360
Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu
1105                1110                1115                1120

GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT GAA TCT AAC      3408
Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn
                1125                1130                1135

AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT GTA ACA AAG      3456
Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys
            1140                1145                1150

GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT GAG ATC GGA      3504
Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly
        1155                1160                1165

GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA CTC CTT ATG      3552
Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met
    1170                1175                1180

GAG GAA                                                             3558
Glu Glu
1185
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1186 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
 1               5                  10                  15

Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr
            20                  25                  30

Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala
        35                  40                  45

Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly
    50                  55                  60

Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu
65                  70                  75                  80

Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser
                85                  90                  95

Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe
            100                 105                 110

Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met
        115                 120                 125

Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro
    130                 135                 140

Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
145                 150                 155                 160

Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
                165                 170                 175

Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
            180                 185                 190

Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
        195                 200                 205

Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
    210                 215                 220
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Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
225                 230                 235                 240

Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
                245                 250                 255

Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
            260                 265                 270

Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
        275                 280                 285

Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
    290                 295                 300

Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
305                 310                 315                 320

Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
                325                 330                 335

Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
            340                 345                 350

Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
        355                 360                 365

Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
    370                 375                 380

Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
385                 390                 395                 400

Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
                405                 410                 415

Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
            420                 425                 430

Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
        435                 440                 445

Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
    450                 455                 460

Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly Gly Thr Ser
465                 470                 475                 480

Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
                485                 490                 495

Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
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            500                 505                 510

Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
        515                 520                 525

Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val Gly Gly Gln
    530                 535                 540

Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile Gly Glu Asn
545                 550                 555                 560

Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn Pro Phe Ser
                565                 570                 575

Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln Pro Leu Phe
            580                 585                 590

Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp Lys Ile Glu
        595                 600                 605

Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg
    610                 615                 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn Gln Ile Gly
625                 630                 635                 640

Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
                645                 650                 655

Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
            660                 665                 670

Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu
        675                 680                 685

Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly
    690                 695                 700

Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe
705                 710                 715                 720

Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro
                725                 730                 735

Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr
            740                 745                 750

Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile
        755                 760                 765

Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly
    770                 775                 780
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Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys
785                 790                 795                 800

Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu
                805                 810                 815

Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His
            820                 825                 830

Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu
        835                 840                 845

Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg
    850                 855                 860

Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala
865                 870                 875                 880

Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu
                885                 890                 895

Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser
            900                 905                 910

Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Val Asp
        915                 920                 925

Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile
    930                 935                 940

Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala
945                 950                 955                 960

Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser Leu
                965                 970                 975

Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu
            980                 985                 990

Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn
        995                 1000                1005

His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln
    1010                1015                1020

Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
1025                1030                1035                1040

Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
                1045                1050                1055

Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val
            1060                1065                1070
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Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly Thr Gln Glu
        1075                1080                1085

Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr Asp Glu Ala
    1090                1095                1100

Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu
1105                1110                1115                1120

Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn
                1125                1130                1135

Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys
            1140                1145                1150

Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly
        1155                1160                1165

Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met
    1170                1175                1180

Glu Glu
1185
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Hybrid toxin

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAT AAT TGT TTA        48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
  1               5                  10                  15
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AGT AAC CCT GAA GTA GAA GTA TTA GGT GGA GAA AGA ATA GAA ACT GGT      96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
            20                  25                  30

TAC ACC CCA ATC GAT ATT TCC TTG TCG CTA ACG CAA TTT CTT TTG AGT     144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
        35                  40                  45

GAA TTT GTT CCC GGT GCT GGA TTT GTG TTA GGA CTA GTT GAT ATA ATA     192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
    50                  55                  60

TGG GGA ATT TTT GGT CCC TCT CAA TGG GAC GCA TTT CTT GTA CAA ATT     240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65                  70                  75                  80

GAA CAG TTA ATT AAC CAA AGA ATA GAA GAA TTC GCT AGG AAC CAA GCC     288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
                85                  90                  95

ATT TCT AGA TTA GAA GGA CTA AGC AAT CTT TAT CAA ATT TAC GCA GAA     336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
            100                 105                 110

TCT TTT AGA GAG TGG GAA GCA GAT CCT ACT AAT CCA GCA TTA AGA GAA     384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
        115                 120                 125

GAG ATG CGT ATT CAA TTC AAT GAC ATG AAC AGT GCC CTT ACA ACC GCT     432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
    130                 135                 140

ATT CCT CTT TTT GCA GTT CAA AAT TAT CAA GTT CCT CTT TTA TCA GTA     480
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145                 150                 155                 160

TAT GTT CAA GCT GCA AAT TTA CAT TTA TCA GTT TTG AGA GAT GTT TCA     528
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
                165                 170                 175

GTG TTT GGA CAA AGG TGG GGA TTT GAT GCC GCG ACT ATC AAT AGT CGT     576
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
            180                 185                 190

TAT AAT GAT TTA ACT AGG CTT ATT GGC AAC TAT ACA GAT CAT GCT GTA     624
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
        195                 200                 205

CGC TGG TAC AAT ACG GGA TTA GAG CGT GTA TGG GGA CCG GAT TCT AGA     672
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
    210                 215                 220

GAT TGG ATA AGA TAT AAT CAA TTT AGA AGA GAA TTA ACA CTA ACT GTA     720
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Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225                 230                 235                 240

TTA GAT ATC GTT TCT CTA TTT CCG AAC TAT GAT AGT AGA ACG TAT CCA      768
Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
                245                 250                 255

ATT CGA ACA GTT TCC CAA TTA ACA AGA GAA ATT TAT ACA AAC CCA GTA      816
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
            260                 265                 270

TTA GAA AAT TTT GAT GGT AGT TTT CGA GGC TCG GCT CAG GGC ATA GAA      864
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
        275                 280                 285

GGA AGT ATT AGG AGT CCA CAT TTG ATG GAT ATA CTT AAC AGT ATA ACC      912
Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
    290                 295                 300

ATC TAT ACG GAT GCT CAT AGA GGA GAA TAT TAT TGG TCA GGG CAT CAA      960
Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305                 310                 315                 320

ATA ATG GCT TCT CCT GTA GGG TTT TCG GGG CCA GAA TTC ACT TTT CCG     1008
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
                325                 330                 335

CTA TAT GGA ACT ATG GGA AAT GCA GCT CCA CAA CAA CGT ATT GTT GCT     1056
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
            340                 345                 350

CAA CTA GGT CAG GGC GTG TAT AGA ACA TTA TCG TCC ACT TTA TAT AGA     1104
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
        355                 360                 365

AGA CCT TTT AAT ATA GGG ATA AAT AAT CAA CAA CTA TCT GTT CTT GAC     1152
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
    370                 375                 380

GGG ACA GAA TTT GCT TAT GGA ACC TCC TCA AAT TTG CCA TCC GCT GTA     1200
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385                 390                 395                 400

TAC AGA AAA AGC GGA ACG GTA GAT TCG CTG GAT GAA ATA CCG CCA CAG     1248
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
                405                 410                 415

AAT AAC AAC GTG CCA CCT AGG CAA GGA TTT AGT CAT CGA TTA AGC CAT     1296
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
            420                 425                 430

GTT TCA ATG TTT CGT TCA GGC TTT AGT AAT AGT AGT GTA AGT ATA ATA     1344
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
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        435                 440                 445

AGA GCT CCT ATG TTC TCT TGG ATA CAT CGT AGT GCA ACT CTT ACA AAT      1392
Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Thr Leu Thr Asn
    450                 455                 460

ACA ATT GAT CCA GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT      1440
Thr Ile Asp Pro Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe
465                 470                 475                 480

AGA GTT TGG GGG GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA      1488
Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
                485                 490                 495

GGG GAT ATC CTT CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA      1536
Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
            500                 505                 510

GTC AAT ATT AAT TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT      1584
Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
        515                 520                 525

TAC GCT TCC AGT AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA      1632
Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
    530                 535                 540

TCC ACA GGA GTG GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA      1680
Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
545                 550                 555                 560

ACT ATG GAA ATA GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC      1728
Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
                565                 570                 575

GAT TTT AGT AAT CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG      1776
Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
            580                 585                 590

ATA AGT GAA CAA CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA      1824
Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
        595                 600                 605

CTT TAT ATA GAT AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA      1872
Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
    610                 615                 620

GCA GAA TCT GAT TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT      1920
Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe
625                 630                 635                 640

ACT TCT TCC AAT CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT      1968
Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His
                645                 650                 655
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ATT GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT      2016
Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys
            660                 665                 670

CTG GAT GAA AAG CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA      2064
Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
        675                 680                 685

CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC      2112
Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
    690                 695                 700

AAT AGA CAA CCA GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC      2160
Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
705                 710                 715                 720

CAA GGA GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT      2208
Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly
                725                 730                 735

ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG      2256
Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
            740                 745                 750

TCG AAA TTA AAA GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA      2304
Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu
        755                 760                 765

GAT AGT CAA GAC TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC      2352
Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
    770                 775                 780

GAA ATA GTA AAT GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC      2400
Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
785                 790                 795                 800

CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC      2448
Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His
                805                 810                 815

CTT GAA TGG AAT CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA      2496
Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys
            820                 825                 830

TGT GCA CAT CAT TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT      2544
Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys
        835                 840                 845

ACA GAC TTA AAT GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG      2592
Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys
    850                 855                 860
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ACG CAA GAT GGC CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG      2640
Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
865                 870                 875                 880

AAA CCA TTA TTA GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG      2688
Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys
                885                 890                 895

AAG TGG AGA GAC AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT      2736
Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val
            900                 905                 910

TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA      2784
Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
        915                 920                 925

TAT GAT AGA TTA CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA      2832
Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala
    930                 935                 940

GAT AAA CGC GTT CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT      2880
Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
945                 950                 955                 960

GTG ATT CCA GGT GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT      2928
Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg
                965                 970                 975

ATT TTT ACA GCG TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT      2976
Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
            980                 985                 990

GGC GAT TTC AAT AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA      3024
Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val
        995                 1000                1005

GAT GTA GAA GAG CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA      3072
Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu
    1010                1015                1020

TGG GAG GCA GAA GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC      3120
Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly
1025                1030                1035                1040

TAT ATC CTT CGT GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC      3168
Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys
                1045                1050                1055

GTA ACG ATC CAT GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC      3216
Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser
            1060                1065                1070

AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT      3264
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Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn
       1075                1080                1085

AAT TAT ACT GGG ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT      3312
Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg
    1090                1095                1100

AAT CAA GGA TAT GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT      3360
Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala
1105                1110                1115                1120

GAT TAC GCT TCA GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA      3408
Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg
                1125                1130                1135

GAG AAT CCT TGT GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA      3456
Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
            1140                1145                1150

CCG GCT GGT TAT GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT      3504
Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp
       1155                1160                1165

AAG GTA TGG ATT GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT      3552
Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
    1170                1175                1180

AGC GTG GAA TTA CTC CTT ATG GAG GAA                                  3579
Ser Val Glu Leu Leu Leu Met Glu Glu
1185                1190
```

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
  1               5                  10                  15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
             20                  25                  30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
         35                  40                  45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
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     50                  55                  60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65                  70                  75                  80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
                85                  90                  95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
            100                 105                 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
        115                 120                 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
    130                 135                 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145                 150                 155                 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
                165                 170                 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
            180                 185                 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
        195                 200                 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
    210                 215                 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225                 230                 235                 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
                245                 250                 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
            260                 265                 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
        275                 280                 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
    290                 295                 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305                 310                 315                 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
                325                 330                 335
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Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
            340                 345                 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
        355                 360                 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
    370                 375                 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385                 390                 395                 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
                405                 410                 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
            420                 425                 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
        435                 440                 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Thr Leu Thr Asn
    450                 455                 460

Thr Ile Asp Pro Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe
465                 470                 475                 480

Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
                485                 490                 495

Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
            500                 505                 510

Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
        515                 520                 525

Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
    530                 535                 540

Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
545                 550                 555                 560

Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
                565                 570                 575

Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
            580                 585                 590

Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
        595                 600                 605

Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
    610                 615                 620
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Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe
625                 630                 635                 640

Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His
                645                 650                 655

Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys
            660                 665                 670

Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
        675                 680                 685

Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
    690                 695                 700

Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
705                 710                 715                 720

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly
                725                 730                 735

Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
            740                 745                 750

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu
        755                 760                 765

Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
    770                 775                 780

Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
785                 790                 795                 800

Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His
                805                 810                 815

Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys
            820                 825                 830

Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys
        835                 840                 845

Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys
    850                 855                 860

Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
865                 870                 875                 880

Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys
                885                 890                 895

Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val
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900 905 910

Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
915 920 925

Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala
930 935 940

Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
945 950 955 960

Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg
965 970 975

Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
980 985 990

Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val
995 1000 1005

Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu
1010 1015 1020

Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly
1025 1030 1035 1040

Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys
1045 1050 1055

Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser
1060 1065 1070

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn
1075 1080 1085

Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg
1090 1095 1100

Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala
1105 1110 1115 1120

Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg
1125 1130 1135

Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
1140 1145 1150

Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp
1155 1160 1165

Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
1170 1175 1180

Ser Val Glu Leu Leu Leu Met Glu Glu
1185 1190

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bacillus thuringiensis

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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ATG AAT CAA AAT AAA CAC GGA ATT ATT GGC GCT TCC AAT TGT GGT TGT      48
Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys
 1               5                  10                  15

GCA TCT GAT GAT GTT GCG AAA TAT CCT TTA GCC AAC AAT CCA TAT TCA      96
Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser
            20                  25                  30

TCT GCT TTA AAT TTA AAT TCT TGT CAA AAT AGT AGT ATT CTC AAC TGG     144
Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp
        35                  40                  45

ATT AAC ATA ATA GGC GAT GCA GCA AAA GAA GCA GTA TCT ATT GGG ACA     192
Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr
    50                  55                  60

ACC ATA GTC TCT CTT ATC ACA GCA CCT TCT CTT ACT GGA TTA ATT TCA     240
Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser
65                  70                  75                  80

ATA GTA TAT GAC CTT ATA GGT AAA GTA CTA GGA GGT AGT AGT GGA CAA     288
Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln
                85                  90                  95

TCC ATA TCA GAT TTG TCT ATA TGT GAC TTA TTA TCT ATT ATT GAT TTA     336
Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu
            100                 105                 110

CGG GTA AGT CAG AGT GTT TTA AAT GAT GGG ATT GCA GAT TTT AAT GGT     384
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Arg Val Ser Gln Ser Val Leu Asn Asp Gly Ile Ala Asp Phe Asn Gly
        115                 120                 125

TCT GTA CTC TTA TAC AGG AAC TAT TTA GAG GCT CTG GAT AGC TGG AAT        432
Ser Val Leu Leu Tyr Arg Asn Tyr Leu Glu Ala Leu Asp Ser Trp Asn
    130                 135                 140

AAG AAT CCT AAT TCT GCT TCT GCT GAA GAA CTC CGT ACT CGT TTT AGA        480
Lys Asn Pro Asn Ser Ala Ser Ala Glu Glu Leu Arg Thr Arg Phe Arg
145                 150                 155                 160

ATC GCC GAC TCA GAA TTT GAT AGA ATT TTA ACC CGA GGG TCT TTA ACG        528
Ile Ala Asp Ser Glu Phe Asp Arg Ile Leu Thr Arg Gly Ser Leu Thr
                165                 170                 175

AAT GGT GGC TCG TTA GCT AGA CAA AAT GCC CAA ATA TTA TTA TTA CCT        576
Asn Gly Gly Ser Leu Ala Arg Gln Asn Ala Gln Ile Leu Leu Leu Pro
            180                 185                 190

TCT TTT GCG AGC GCT GCA TTT TTC CAT TTA TTA CTA CTA AGG GAT GCT        624
Ser Phe Ala Ser Ala Ala Phe Phe His Leu Leu Leu Leu Arg Asp Ala
        195                 200                 205

ACT AGA TAT GGC ACT AAT TGG GGG CTA TAC AAT GCT ACA CCT TTT ATA        672
Thr Arg Tyr Gly Thr Asn Trp Gly Leu Tyr Asn Ala Thr Pro Phe Ile
    210                 215                 220

AAT TAT CAA TCA AAA CTA GTA GAG CTT ATT GAA CTA TAT ACT GAT TAT        720
Asn Tyr Gln Ser Lys Leu Val Glu Leu Ile Glu Leu Tyr Thr Asp Tyr
225                 230                 235                 240

TGC GTA CAT TGG TAT AAT CGA GGT TTC AAC GAA CTA AGA CAA CGA GGC        768
Cys Val His Trp Tyr Asn Arg Gly Phe Asn Glu Leu Arg Gln Arg Gly
                245                 250                 255

ACT AGT GCT ACA GCT TGG TTA GAA TTT CAT AGA TAT CGT AGA GAG ATG        816
Thr Ser Ala Thr Ala Trp Leu Glu Phe His Arg Tyr Arg Arg Glu Met
            260                 265                 270

ACA TTG ATG GTA TTA GAT ATA GTA GCA TCA TTT TCA AGT CTT GAT ATT        864
Thr Leu Met Val Leu Asp Ile Val Ala Ser Phe Ser Ser Leu Asp Ile
        275                 280                 285

ACT AAT TAC CCA ATA GAA ACA GAT TTT CAG TTG AGT AGG GTC ATT TAT        912
Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr
    290                 295                 300

ACA GAT CCA ATT GGT TTT GTA CAT CGT AGT AGT CTT AGG GGA GAA AGT        960
Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser
305                 310                 315                 320

TGG TTT AGC TTT GTT AAT AGA GCT AAT TTC TCA GAT TTA GAA AAT GCA       1008
Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala
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                325                 330                 335

ATA CCT AAT CCT AGA CCG TCT TGG TTT TTA AAT AAT ATG ATT ATA TCT      1056
Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser
            340                 345                 350

ACT GGT TCA CTT ACA TTG CCG GTT AGC CCA AGT ACT GAT AGA GCG AGG      1104
Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg
        355                 360                 365

GTA TGG TAT GGA AGT CGA GAT CGA ATT TCC CCT GCT AAT TCA CAA TTT      1152
Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe
    370                 375                 380

ATT ACT GAA CTA ATC TCT GGA CAA CAT ACG ACT GCT ACA CAA ACT ATT      1200
Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile
385                 390                 395                 400

TTA GGG CGA AAT ATA TTT AGA GTA GAT TCT CAA GCT TGT AAT TTA AAT      1248
Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn
                405                 410                 415

GAT ACC ACA TAT GGA GTG AAT AGG GCG GTA TTT TAT CAT GAT GCG AGT      1296
Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser
            420                 425                 430

GAA GGT TCT CAA AGA TCC GTG TAC GAG GGG TAT ATT CGA ACA ACT GGG      1344
Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly
        435                 440                 445

ATA GAT AAC CCT AGA GTT CAA AAT ATT AAC ACT TAT TTA CCT GGA GAA      1392
Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu
    450                 455                 460

AAT TCA GAT ATC CCA ACT CCA GAA GAC TAT ACT CAT ATA TTA AGC ACA      1440
Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr
465                 470                 475                 480

ACA ATA AAT TTA ACA GGA GGA CTT AGA CAA GTA GCA TCT AAT CGC CGT      1488
Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg
                485                 490                 495

TCA TCT TTA GTA ATG TAT GGT TGG ACA CAT AAA AGT CTG GCT CGT AAC      1536
Ser Ser Leu Val Met Tyr Gly Trp Thr His Lys Ser Leu Ala Arg Asn
            500                 505                 510

AAT ACC ATT AAT CCA GAT AGA ATT ACA CAG ATA CCA TTG ACG AAG GTT      1584
Asn Thr Ile Asn Pro Asp Arg Ile Thr Gln Ile Pro Leu Thr Lys Val
        515                 520                 525

GAT ACC CGA GGC ACA GGT GTT TCT TAT GTG AAT GAT CCA GGA TTT ATA      1632
Asp Thr Arg Gly Thr Gly Val Ser Tyr Val Asn Asp Pro Gly Phe Ile
    530                 535                 540
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GGA GGA GCT CTA CTT CAA AGG ACT GAC CAT GGT TCG CTT GGA GTA TTG      1680
Gly Gly Ala Leu Leu Gln Arg Thr Asp His Gly Ser Leu Gly Val Leu
545                 550                 555                 560

AGG GTC CAA TTT CCA CTT CAC TTA AGA CAA CAA TAT CGT ATT AGA GTC      1728
Arg Val Gln Phe Pro Leu His Leu Arg Gln Gln Tyr Arg Ile Arg Val
                565                 570                 575

CGT TAT GCT TCT ACA ACA AAT ATT CGA TTG AGT GTG AAT GGC AGT TTC      1776
Arg Tyr Ala Ser Thr Thr Asn Ile Arg Leu Ser Val Asn Gly Ser Phe
            580                 585                 590

GGT ACT ATT TCT CAA AAT CTC CCT AGT ACA ATG AGA TTA GGA GAG GAT      1824
Gly Thr Ile Ser Gln Asn Leu Pro Ser Thr Met Arg Leu Gly Glu Asp
        595                 600                 605

TTA AGA TAC GGA TCT TTT GCT ATA AGA GAG TTT AAT ACT TCT ATT AGA      1872
Leu Arg Tyr Gly Ser Phe Ala Ile Arg Glu Phe Asn Thr Ser Ile Arg
    610                 615                 620

CCC ACT GCA AGT CCG GAC CAA ATT CGA TTG ACA ATA GAA CCA TCT TTT      1920
Pro Thr Ala Ser Pro Asp Gln Ile Arg Leu Thr Ile Glu Pro Ser Phe
625                 630                 635                 640

ATT AGA CAA GAG GTC TAT GTA GAT AGA ATT GAG TTC ATT CCA GTT AAT      1968
Ile Arg Gln Glu Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asn
                645                 650                 655

CCG ACG CGA GAG GCG AAA GAG GAT CTA GAA GCA GCA AAA AAA GCG GTG      2016
Pro Thr Arg Glu Ala Lys Glu Asp Leu Glu Ala Ala Lys Lys Ala Val
            660                 665                 670

GCG AGC TTG TTT ACA CGC ACA AGG GAC GGA TTA CAA GTA AAT GTG AAA      2064
Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn Val Lys
        675                 680                 685

GAT TAT CAA GTC GAT CAA GCG GCA AAT TTA GTG TCA TGC TTA TCA GAT      2112
Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu Ser Asp
    690                 695                 700

GAA CAA TAT GGG TAT GAC AAA AAG ATG TTA TTG GAA GCG GTA CGT GCG      2160
Glu Gln Tyr Gly Tyr Asp Lys Lys Met Leu Leu Glu Ala Val Arg Ala
705                 710                 715                 720

GCA AAA CGA CTT AGC CGA GAA CGC AAC TTA CTT CAG GAT CCA GAT TTT      2208
Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro Asp Phe
                725                 730                 735

AAT ACA ATC AAT AGT ACA GAA GAA AAT GGA TGG AAA GCA AGT AAC GGC      2256
Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser Asn Gly
            740                 745                 750
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GTT ACT ATT AGT GAG GGC GGG CCA TTC TAT AAA GGC CGT GCA ATT CAG      2304
Val Thr Ile Ser Glu Gly Gly Pro Phe Tyr Lys Gly Arg Ala Ile Gln
        755                 760                 765

CTA GCA AGT GCA CGA GAA AAT TAC CCA ACA TAC ATC TAT CAA AAA GTA      2352
Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln Lys Val
    770                 775                 780

GAT GCA TCG GAG TTA AAG CCG TAT ACA CGT TAT AGA CTG GAT GGG TTC      2400
Asp Ala Ser Glu Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp Gly Phe
785                 790                 795                 800

GTG AAG AGT AGT CAA GAT TTA GAA ATT GAT CTC ATT CAC CAT CAT AAA      2448
Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His His Lys
                805                 810                 815

GTC CAT CTT GTG AAA AAT GTA CCA GAT AAT TTA GTA TCT GAT ACT TAC      2496
Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp Thr Tyr
            820                 825                 830

CCA GAT GAT TCT TGT AGT GGA ATC AAT CGA TGT CAG GAA CAA CAG ATG      2544
Pro Asp Asp Ser Cys Ser Gly Ile Asn Arg Cys Gln Glu Gln Gln Met
        835                 840                 845

GTA AAT GCG CAA CTG GAA ACA GAG CAT CAT CAT CCG ATG GAT TGC TGT      2592
Val Asn Ala Gln Leu Glu Thr Glu His His His Pro Met Asp Cys Cys
    850                 855                 860

GAA GCA GCT CAA ACA CAT GAG TTT TCT TCC TAT ATT GAT ACA GGG GAT      2640
Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asp Thr Gly Asp
865                 870                 875                 880

TTA AAT TCG AGT GTA GAC CAG GGA ATC TGG GCG ATC TTT AAA GTT CGA      2688
Leu Asn Ser Ser Val Asp Gln Gly Ile Trp Ala Ile Phe Lys Val Arg
                885                 890                 895

ACA ACC GAT GGT TAT GCG ACG TTA GGA AAT CTT GAA TTG GTA GAG GTC      2736
Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Val
            900                 905                 910

GGA CCG TTA TCG GGT GAA TCT TTA GAA CGT GAA CAA AGG GAT AAT ACA      2784
Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn Thr
        915                 920                 925

AAA TGG AGT GCA GAG CTA GGA AGA AAG CGT GCA GAA ACA GAT CGC GTG      2832
Lys Trp Ser Ala Glu Leu Gly Arg Lys Arg Ala Glu Thr Asp Arg Val
    930                 935                 940

TAT CAA GAT GCC AAA CAA TCC ATC AAT CAT TTA TTT GTG GAT TAT CAA      2880
Tyr Gln Asp Ala Lys Gln Ser Ile Asn His Leu Phe Val Asp Tyr Gln
945                 950                 955                 960

GAT CAA CAA TTA AAT CCA GAA ATA GGG ATG GCA GAT ATT ATG GAC GCT      2928
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Asp Gln Gln Leu Asn Pro Glu Ile Gly Met Ala Asp Ile Met Asp Ala
                965                 970                 975

CAA AAT CTT GTC GCA TCA ATT TCA GAT GTA TAT AGC GAT GCC GTA CTG      2976
Gln Asn Leu Val Ala Ser Ile Ser Asp Val Tyr Ser Asp Ala Val Leu
            980                 985                 990

CAA ATC CCT GGA ATT AAC TAT GAG ATT TAC ACA GAG CTG TCC AAT CGC      3024
Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asn Arg
        995                 1000                1005

TTA CAA CAA GCA TCG TAT CTG TAT ACG TCT CGA AAT GCG GTG CAA AAT      3072
Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val Gln Asn
    1010                1015                1020

GGG GAC TTT AAC AAC GGG CTA GAT AGC TGG AAT GCA ACA GCG GGT GCA      3120
Gly Asp Phe Asn Asn Gly Leu Asp Ser Trp Asn Ala Thr Ala Gly Ala
1025                1030                1035                1040

TCG GTA CAA CAG GAT GGC AAT ACG CAT TTC TTA GTT CTT TCT CAT TGG      3168
Ser Val Gln Gln Asp Gly Asn Thr His Phe Leu Val Leu Ser His Trp
                1045                1050                1055

GAT GCA CAA GTT TCT CAA CAA TTT AGA GTG CAG CCG AAT TGT AAA TAT      3216
Asp Ala Gln Val Ser Gln Gln Phe Arg Val Gln Pro Asn Cys Lys Tyr
            1060                1065                1070

GTA TTA CGT GTA ACA GCA GAG AAA GTA GGC GGC GGA GAC GGA TAC GTG      3264
Val Leu Arg Val Thr Ala Glu Lys Val Gly Gly Gly Asp Gly Tyr Val
        1075                1080                1085

ACT ATC CGG GAT GAT GCT CAT CAT ACA GAA ACG CTT ACA TTT AAT GCA      3312
Thr Ile Arg Asp Asp Ala His His Thr Glu Thr Leu Thr Phe Asn Ala
    1090                1095                1100

TGT GAT TAT GAT ATA AAT GGC ACG TAC GTG ACT GAT AAT ACG TAT CTA      3360
Cys Asp Tyr Asp Ile Asn Gly Thr Tyr Val Thr Asp Asn Thr Tyr Leu
1105                1110                1115                1120

ACA AAA GAA GTG GTA TTC CAT CCG GAG ACA CAA CAC ATG TGG GTA GAG      3408
Thr Lys Glu Val Val Phe His Pro Glu Thr Gln His Met Trp Val Glu
                1125                1130                1135

GTA AAT GAA ACA GAA GGT GCA TTT CAT ATA GAT AGT ATT GAA TTC GTT      3456
Val Asn Glu Thr Glu Gly Ala Phe His Ile Asp Ser Ile Glu Phe Val
            1140                1145                1150

GAA ACA GAA AAG                                                     3468
Glu Thr Glu Lys
        1155
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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1156 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys
 1               5                  10                  15

Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser
            20                  25                  30

Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp
        35                  40                  45

Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr
    50                  55                  60

Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser
65                  70                  75                  80

Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln
                85                  90                  95

Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu
            100                 105                 110

Arg Val Ser Gln Ser Val Leu Asn Asp Gly Ile Ala Asp Phe Asn Gly
        115                 120                 125

Ser Val Leu Leu Tyr Arg Asn Tyr Leu Glu Ala Leu Asp Ser Trp Asn
    130                 135                 140

Lys Asn Pro Asn Ser Ala Ser Ala Glu Glu Leu Arg Thr Arg Phe Arg
145                 150                 155                 160

Ile Ala Asp Ser Glu Phe Asp Arg Ile Leu Thr Arg Gly Ser Leu Thr
                165                 170                 175

Asn Gly Gly Ser Leu Ala Arg Gln Asn Ala Gln Ile Leu Leu Leu Pro
            180                 185                 190

Ser Phe Ala Ser Ala Ala Phe Phe His Leu Leu Leu Leu Arg Asp Ala
        195                 200                 205

Thr Arg Tyr Gly Thr Asn Trp Gly Leu Tyr Asn Ala Thr Pro Phe Ile
    210                 215                 220

Asn Tyr Gln Ser Lys Leu Val Glu Leu Ile Glu Leu Tyr Thr Asp Tyr
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225 230 235 240

Cys Val His Trp Tyr Asn Arg Gly Phe Asn Glu Leu Arg Gln Arg Gly
245 250 255

Thr Ser Ala Thr Ala Trp Leu Glu Phe His Arg Tyr Arg Arg Glu Met
260 265 270

Thr Leu Met Val Leu Asp Ile Val Ala Ser Phe Ser Ser Leu Asp Ile
275 280 285

Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr
290 295 300

Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser
305 310 315 320

Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala
325 330 335

Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser
340 345 350

Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg
355 360 365

Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe
370 375 380

Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile
385 390 395 400

Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn
405 410 415

Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser
420 425 430

Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly
435 440 445

Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu
450 455 460

Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr
465 470 475 480

Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg
485 490 495

Ser Ser Leu Val Met Tyr Gly Trp Thr His Lys Ser Leu Ala Arg Asn
500 505 510

Asn Thr Ile Asn Pro Asp Arg Ile Thr Gln Ile Pro Leu Thr Lys Val
515 520 525

Asp Thr Arg Gly Thr Gly Val Ser Tyr Val Asn Asp Pro Gly Phe Ile
530 535 540

Gly Gly Ala Leu Leu Gln Arg Thr Asp His Gly Ser Leu Gly Val Leu
545 550 555 560

Arg Val Gln Phe Pro Leu His Leu Arg Gln Gln Tyr Arg Ile Arg Val
565 570 575

Arg Tyr Ala Ser Thr Thr Asn Ile Arg Leu Ser Val Asn Gly Ser Phe
580 585 590

Gly Thr Ile Ser Gln Asn Leu Pro Ser Thr Met Arg Leu Gly Glu Asp
595 600 605

Leu Arg Tyr Gly Ser Phe Ala Ile Arg Glu Phe Asn Thr Ser Ile Arg
610 615 620

Pro Thr Ala Ser Pro Asp Gln Ile Arg Leu Thr Ile Glu Pro Ser Phe
625 630 635 640

Ile Arg Gln Glu Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asn
645 650 655

Pro Thr Arg Glu Ala Lys Glu Asp Leu Glu Ala Ala Lys Lys Ala Val
660 665 670

Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn Val Lys
675 680 685

Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu Ser Asp
690 695 700

Glu Gln Tyr Gly Tyr Asp Lys Lys Met Leu Leu Glu Ala Val Arg Ala
705 710 715 720

Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro Asp Phe
725 730 735

Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser Asn Gly
740 745 750

Val Thr Ile Ser Glu Gly Gly Pro Phe Tyr Lys Gly Arg Ala Ile Gln
755 760 765

Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln Lys Val
770 775 780

Asp Ala Ser Glu Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp Gly Phe
785 790 795 800

Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His His Lys
805 810 815

Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp Thr Tyr
820 825 830

Pro Asp Asp Ser Cys Ser Gly Ile Asn Arg Cys Gln Glu Gln Gln Met
835 840 845

Val Asn Ala Gln Leu Glu Thr Glu His His His Pro Met Asp Cys Cys
850 855 860

Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asp Thr Gly Asp
865 870 875 880

Leu Asn Ser Ser Val Asp Gln Gly Ile Trp Ala Ile Phe Lys Val Arg
885 890 895

Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Val
900 905 910

Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn Thr
915 920 925

Lys Trp Ser Ala Glu Leu Gly Arg Lys Arg Ala Glu Thr Asp Arg Val
930 935 940

Tyr Gln Asp Ala Lys Gln Ser Ile Asn His Leu Phe Val Asp Tyr Gln
945 950 955 960

Asp Gln Gln Leu Asn Pro Glu Ile Gly Met Ala Asp Ile Met Asp Ala
965 970 975

Gln Asn Leu Val Ala Ser Ile Ser Asp Val Tyr Ser Asp Ala Val Leu
980 985 990

Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asn Arg
995 1000 1005

Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val Gln Asn
1010 1015 1020

Gly Asp Phe Asn Asn Gly Leu Asp Ser Trp Asn Ala Thr Ala Gly Ala
1025 1030 1035 1040

Ser Val Gln Gln Asp Gly Asn Thr His Phe Leu Val Leu Ser His Trp
1045 1050 1055

Asp Ala Gln Val Ser Gln Gln Phe Arg Val Gln Pro Asn Cys Lys Tyr
1060 1065 1070

Val Leu Arg Val Thr Ala Glu Lys Val Gly Gly Gly Asp Gly Tyr Val

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        1075                1080                1085

Thr Ile Arg Asp Asp Ala His His Thr Glu Thr Leu Thr Phe Asn Ala
    1090                1095                1100

Cys Asp Tyr Asp Ile Asn Gly Thr Tyr Val Thr Asp Asn Thr Tyr Leu
1105                1110                1115                1120

Thr Lys Glu Val Val Phe His Pro Glu Thr Gln His Met Trp Val Glu
                1125                1130                1135

Val Asn Glu Thr Glu Gly Ala Phe His Ile Asp Ser Ile Glu Phe Val
            1140                1145                1150

Glu Thr Glu Lys
        1155
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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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ATG AAT CAA AAT AAA CAC GGA ATT ATT GGC GCT TCC AAT TGT GGT TGT      48
Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys
  1               5                  10                  15

GCA TCT GAT GAT GTT GCG AAA TAT CCT TTA GCC AAC AAT CCA TAT TCA      96
Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser
            20                  25                  30

TCT GCT TTA AAT TTA AAT TCT TGT CAA AAT AGT AGT ATT CTC AAC TGG     144
Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp
        35                  40                  45

ATT AAC ATA ATA GGC GAT GCA GCA AAA GAA GCA GTA TCT ATT GGG ACA     192
Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr
    50                  55                  60

ACC ATA GTC TCT CTT ATC ACA GCA CCT TCT CTT ACT GGA TTA ATT TCA     240
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Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser
 65                  70                  75                  80

ATA GTA TAT GAC CTT ATA GGT AAA GTA CTA GGA GGT AGT AGT GGA CAA      288
Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln
                 85                  90                  95

TCC ATA TCA GAT TTG TCT ATA TGT GAC TTA TTA TCT ATT ATT GAT TTA      336
Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu
            100                 105                 110

CGG GTA AGT CAG AGT GTT TTA AAT GAT GGG ATT GCA GAT TTT AAT GGT      384
Arg Val Ser Gln Ser Val Leu Asn Asp Gly Ile Ala Asp Phe Asn Gly
        115                 120                 125

TCT GTA CTC TTA TAC AGG AAC TAT TTA GAG GCT CTG GAT AGC TGG AAT      432
Ser Val Leu Leu Tyr Arg Asn Tyr Leu Glu Ala Leu Asp Ser Trp Asn
    130                 135                 140

AAG AAT CCT AAT TCT GCT TCT GCT GAA GAA CTC CGT ACT CGT TTT AGA      480
Lys Asn Pro Asn Ser Ala Ser Ala Glu Glu Leu Arg Thr Arg Phe Arg
145                 150                 155                 160

ATC GCC GAC TCA GAA TTT GAT AGA ATT TTA ACC CGA GGG TCT TTA ACG      528
Ile Ala Asp Ser Glu Phe Asp Arg Ile Leu Thr Arg Gly Ser Leu Thr
                165                 170                 175

AAT GGT GGC TCG TTA GCT AGA CAA AAT GCC CAA ATA TTA TTA TTA CCT      576
Asn Gly Gly Ser Leu Ala Arg Gln Asn Ala Gln Ile Leu Leu Leu Pro
            180                 185                 190

TCT TTT GCG AGC GCT GCA TTT TTC CAT TTA TTA CTA CTA AGG GAT GCT      624
Ser Phe Ala Ser Ala Ala Phe Phe His Leu Leu Leu Leu Arg Asp Ala
        195                 200                 205

ACT AGA TAT GGC ACT AAT TGG GGG CTA TAC AAT GCT ACA CCT TTT ATA      672
Thr Arg Tyr Gly Thr Asn Trp Gly Leu Tyr Asn Ala Thr Pro Phe Ile
    210                 215                 220

AAT TAT CAA TCA AAA CTA GTA GAG CTT ATT GAA CTA TAT ACT GAT TAT      720
Asn Tyr Gln Ser Lys Leu Val Glu Leu Ile Glu Leu Tyr Thr Asp Tyr
225                 230                 235                 240

TGC GTA CAT TGG TAT AAT CGA GGT TTC AAC GAA CTA AGA CAA CGA GGC      768
Cys Val His Trp Tyr Asn Arg Gly Phe Asn Glu Leu Arg Gln Arg Gly
                245                 250                 255

ACT AGT GCT ACA GCT TGG TTA GAA TTT CAT AGA TAT CGT AGA GAG ATG      816
Thr Ser Ala Thr Ala Trp Leu Glu Phe His Arg Tyr Arg Arg Glu Met
            260                 265                 270

ACA TTG ATG GTA TTA GAT ATA GTA GCA TCA TTT TCA AGT CTT GAT ATT      864
Thr Leu Met Val Leu Asp Ile Val Ala Ser Phe Ser Ser Leu Asp Ile
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        275                 280                 285

ACT AAT TAC CCA ATA GAA ACA GAT TTT CAG TTG AGT AGG GTC ATT TAT      912
Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr
    290                 295                 300

ACA GAT CCA ATT GGT TTT GTA CAT CGT AGT AGT CTT AGG GGA GAA AGT      960
Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser
305                 310                 315                 320

TGG TTT AGC TTT GTT AAT AGA GCT AAT TTC TCA GAT TTA GAA AAT GCA      1008
Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala
                325                 330                 335

ATA CCT AAT CCT AGA CCG TCT TGG TTT TTA AAT AAT ATG ATT ATA TCT      1056
Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser
            340                 345                 350

ACT GGT TCA CTT ACA TTG CCG GTT AGC CCA AGT ACT GAT AGA GCG AGG      1104
Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg
        355                 360                 365

GTA TGG TAT GGA AGT CGA GAT CGA ATT TCC CCT GCT AAT TCA CAA TTT      1152
Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe
    370                 375                 380

ATT ACT GAA CTA ATC TCT GGA CAA CAT ACG ACT GCT ACA CAA ACT ATT      1200
Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile
385                 390                 395                 400

TTA GGG CGA AAT ATA TTT AGA GTA GAT TCT CAA GCT TGT AAT TTA AAT      1248
Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn
                405                 410                 415

GAT ACC ACA TAT GGA GTG AAT AGG GCG GTA TTT TAT CAT GAT GCG AGT      1296
Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser
            420                 425                 430

GAA GGT TCT CAA AGA TCC GTG TAC GAG GGG TAT ATT CGA ACA ACT GGG      1344
Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly
        435                 440                 445

ATA GAT AAC CCT AGA GTT CAA AAT ATT AAC ACT TAT TTA CCT GGA GAA      1392
Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu
    450                 455                 460

AAT TCA GAT ATC CCA ACT CCA GAA GAC TAT ACT CAT ATA TTA AGC ACA      1440
Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr
465                 470                 475                 480

ACA ATA AAT TTA AGA GGA GGA CTT AGA CAA GTA GCA TCT AAT CGC CGT      1488
Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg
                485                 490                 495
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TCA TCT TTA GTA ATG TAT GGT TGG ACA CAT AAA AGT CTG GCT CGT AAC      1536
Ser Ser Leu Val Met Tyr Gly Trp Thr His Lys Ser Leu Ala Arg Asn
            500                 505                 510

AAT ACC ATT AAT CCA GAT AGA ATT ACA CAG ATA CCT TTA GTG AAA GGA      1584
Asn Thr Ile Asn Pro Asp Arg Ile Thr Gln Ile Pro Leu Val Lys Gly
        515                 520                 525

TTT AGA GTT TGG GGG GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA      1632
Phe Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr
    530                 535                 540

GGA GGG GAT ATC CTT CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA      1680
Gly Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu
545                 550                 555                 560

CAA GTC AAT ATT AAT TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT      1728
Gln Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe
                565                 570                 575

CGT TAC GCT TCC AGT AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG      1776
Arg Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala
            580                 585                 590

GCA TCC ACA GGA GTG GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG      1824
Ala Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln
        595                 600                 605

AAA ACT ATG GAA ATA GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT      1872
Lys Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr
    610                 615                 620

ACC GAT TTT AGT AAT CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT      1920
Thr Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile
625                 630                 635                 640

GGG ATA AGT GAA CAA CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT      1968
Gly Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly
                645                 650                 655

GAA CTT TAT ATA GAT AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT      2016
Glu Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe
            660                 665                 670

GAA GCA GAA TCT GAT TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG      2064
Glu Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu
        675                 680                 685

TTT ACT TCT TCC AAT CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT      2112
Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr
    690                 695                 700
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CAT ATT GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT      2160
His Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe
705                 710                 715                 720

TGT CTG GAT GAA AAG CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG      2208
Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys
                725                 730                 735

CGA CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG      2256
Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly
            740                 745                 750

ATC AAT AGA CAA CCA GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC      2304
Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr
        755                 760                 765

ATC CAA GGA GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG      2352
Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro
    770                 775                 780

GGT ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT      2400
Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp
785                 790                 795                 800

GAG TCG AAA TTA AAA GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC      2448
Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile
                805                 810                 815

GAA GAT AGT CAA GAC TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA      2496
Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys
            820                 825                 830

CAC GAA ATA GTA AAT GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA      2544
His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser
        835                 840                 845

GCC CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA      2592
Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro
    850                 855                 860

CAC CTT GAA TGG AAT CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA      2640
His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu
865                 870                 875                 880

AAA TGT GCA CAT CAT TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA      2688
Lys Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly
                885                 890                 895

TGT ACA GAC TTA AAT GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT      2736
Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile
            900                 905                 910

AAG ACG CAA GAT GGC CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA      2784
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Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu
        915                 920                 925

GAG AAA CCA TTA TTA GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG      2832
Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu
    930                 935                 940

AAG AAG TGG AGA GAC AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT      2880
Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile
945                 950                 955                 960

GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT      2928
Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser
                965                 970                 975

CAA TAT GAT AGA TTA CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG      2976
Gln Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala
            980                 985                 990

GCA GAT AAA CGC GTT CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG      3024
Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu
        995                 1000                1005

TCT GTG ATT CCA GGT GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA      3072
Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly
    1010                1015                1020

CGT ATT TTT ACA GCG TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA      3120
Arg Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys
1025                1030                1035                1040

AAT GGC GAT TTC AAT AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT      3168
Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His
                1045                1050                1055

GTA GAT GTA GAA GAG CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA      3216
Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro
            1060                1065                1070

GAA TGG GAG GCA GAA GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT      3264
Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
        1075                1080                1085

GGC TAT ATC CTT CGT GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC      3312
Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly
    1090                1095                1100

TGC GTA ACG ATC CAT GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC      3360
Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe
1105                1110                1115                1120

AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT      3408
Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
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                1125                1130                1135

AAT AAT TAT ACT GGG ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT      3456
Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
            1140                1145                1150

CGT AAT CAA GGA TAT GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA      3504
Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro
        1155                1160                1165

GCT GAT TAC GCT TCA GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA      3552
Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
    1170                1175                1180

AGA GAG AAT CCT TGT GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA      3600
Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro
1185                1190                1195                1200

CTA CCG GCT GGT TAT GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC      3648
Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr
                1205                1210                1215

GAT AAG GTA TGG ATT GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG      3696
Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
            1220                1225                1230

GAT AGC GTG GAA TTA CTC CTT ATG GAG GAA                              3726
Asp Ser Val Glu Leu Leu Leu Met Glu Glu
        1235                1240
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1242 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys
  1               5                  10                  15

Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser
             20                  25                  30

Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp
         35                  40                  45

Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr
     50                  55                  60
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Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser
 65                  70                  75                  80

Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln
                85                  90                  95

Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu
            100                 105                 110

Arg Val Ser Gln Ser Val Leu Asn Asp Gly Ile Ala Asp Phe Asn Gly
        115                 120                 125

Ser Val Leu Leu Tyr Arg Asn Tyr Leu Glu Ala Leu Asp Ser Trp Asn
    130                 135                 140

Lys Asn Pro Asn Ser Ala Ser Ala Glu Glu Leu Arg Thr Arg Phe Arg
145                 150                 155                 160

Ile Ala Asp Ser Glu Phe Asp Arg Ile Leu Thr Arg Gly Ser Leu Thr
                165                 170                 175

Asn Gly Gly Ser Leu Ala Arg Gln Asn Ala Gln Ile Leu Leu Leu Pro
            180                 185                 190

Ser Phe Ala Ser Ala Ala Phe Phe His Leu Leu Leu Leu Arg Asp Ala
        195                 200                 205

Thr Arg Tyr Gly Thr Asn Trp Gly Leu Tyr Asn Ala Thr Pro Phe Ile
    210                 215                 220

Asn Tyr Gln Ser Lys Leu Val Glu Leu Ile Glu Leu Tyr Thr Asp Tyr
225                 230                 235                 240

Cys Val His Trp Tyr Asn Arg Gly Phe Asn Glu Leu Arg Gln Arg Gly
                245                 250                 255

Thr Ser Ala Thr Ala Trp Leu Glu Phe His Arg Tyr Arg Arg Glu Met
            260                 265                 270

Thr Leu Met Val Leu Asp Ile Val Ala Ser Phe Ser Ser Leu Asp Ile
        275                 280                 285

Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr
    290                 295                 300

Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser
305                 310                 315                 320

Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala
                325                 330                 335

Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser
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            340                 345                 350

Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg
        355                 360                 365

Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe
    370                 375                 380

Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile
385                 390                 395                 400

Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn
                405                 410                 415

Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser
            420                 425                 430

Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly
        435                 440                 445

Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu
    450                 455                 460

Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr
465                 470                 475                 480

Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg
                485                 490                 495

Ser Ser Leu Val Met Tyr Gly Trp Thr His Lys Ser Leu Ala Arg Asn
            500                 505                 510

Asn Thr Ile Asn Pro Asp Arg Ile Thr Gln Ile Pro Leu Val Lys Gly
        515                 520                 525

Phe Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr
    530                 535                 540

Gly Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu
545                 550                 555                 560

Gln Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe
                565                 570                 575

Arg Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala
            580                 585                 590

Ala Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln
        595                 600                 605

Lys Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr
    610                 615                 620
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Thr Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile
625                 630                 635                 640

Gly Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly
                645                 650                 655

Glu Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe
            660                 665                 670

Glu Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu
        675                 680                 685

Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr
    690                 695                 700

His Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe
705                 710                 715                 720

Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys
                725                 730                 735

Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly
            740                 745                 750

Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr
        755                 760                 765

Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro
    770                 775                 780

Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp
785                 790                 795                 800

Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile
                805                 810                 815

Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys
            820                 825                 830

His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser
        835                 840                 845

Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro
    850                 855                 860

His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu
865                 870                 875                 880

Lys Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly
                885                 890                 895

Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile
            900                 905                 910
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Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu
915 920 925

Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu
930 935 940

Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile
945 950 955 960

Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser
965 970 975

Gln Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala
980 985 990

Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu
995 1000 1005

Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly
1010 1015 1020

Arg Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys
1025 1030 1035 1040

Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His
1045 1050 1055

Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro
1060 1065 1070

Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
1075 1080 1085

Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly
1090 1095 1100

Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe
1105 1110 1115 1120

Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
1125 1130 1135

Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
1140 1145 1150

Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro
1155 1160 1165

Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
1170 1175 1180

Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro

1185 1190 1195 1200

Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr
1205 1210 1215

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
1220 1225 1230

Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1235 1240

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "BglII site downstream of translation termination codon of CryIC."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATAAGATCTG TT 12

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTAGCCATG GATCAAAATA AACACGGAAT TATTG 35

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGGTCAGAT CTTTGAAGTA GAGCTCC 27